

## SEQUENCE LISTING

- <110> Genentech, Inc.  
Ashkenazi, Avi  
Botstein, David  
Desnoyers, Luc  
Eaton, Dan L.  
Ferrara, Napoleone  
Filvaroff, Ellen  
Fong, Sherman  
Gao, Wei-Qiang  
Gerber, Hanspeter  
Gerritsen, Mary E.  
Goddard, A.  
Godowski, Paul J.  
Grimaldi, Christopher J.  
Gurney, Austin L.  
Hillan, Kenneth, J.  
Kljavin, Ivar J.  
Mather, Jennie P.  
Pan, James  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Stewart, Timothy A.  
Tumas, Daniel  
Williams, P. Mickey  
Wood, William, I.
- <120> Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same
- <130> 10466-14
- <140> 09/665,350  
<141> 2000-09-18
- <150> PCT/US00/04414  
<151> 2000-02-22
- <150> US 60/143,048  
<151> 1999-07-07
- <150> US 60/145,698  
<151> 1999-07-26
- <150> US 60/146,222  
<151> 1999-07-28
- <150> PCT/US99/20594  
<151> 1999-09-08
- <150> PCT/US99/20944  
<151> 1999-09-13

PCT/US99/20944

<150> PCT/US99/21090  
<151> 1999-09-15

<150> PCT/US99/21547  
<151> 1999-09-15

<150> PCT/US99/23089  
<151> 1999-10-05

<150> PCT/US99/28214  
<151> 1999-11-29

<150> PCT/US99/28313  
<151> 1999-11-30

<150> PCT/US99/28564  
<151> 1999-12-02

<150> PCT/US99/28565  
<151> 1999-12-02

<150> PCT/US99/30095  
<151> 1999-12-16

<150> PCT/US99/30911  
<151> 1999-12-20

<150> PCT/US99/30999  
<151> 1999-12-20  
<150> PCT/US00/00219  
<151> 2000-01-05

<160> 423

<210> 1  
<211> 1825  
<212> DNA  
<213> Homo sapiens

<400> 1  
actgcacctc ggttctatcg attgaattcc ccgggggatcc tctagagatc cctcgacctc 60  
gacccacgcg tccggggccgg agcagcacgg ccgcaggacc tggagctccg gctgcgtctt 120  
cccgcagcgc taccgcgccat gcgcctgccg ccgcggggccg cgctggggct cctgccgctt 180  
ctgctgctgc tgccgcccgc gccggaggcc gccaaagaagc cgacgccctg ccaccggtgc 240  
cgggggctgg tggacaagtt taaccagggg atggtggaca ccgcaaagaa gaactttggc 300  
ggcgggaaca cggttgggga ggaaaagacg ctgtccaagt acgagtccag cgagattcgc 360  
ctgctggaga tcctggaggg gctgtgcgag agcagcgact tcgaatgcaa tcagatgcta 420  
gaggcgcagg aggagcacct ggaggcctgg tggctgcagc tgaagagcga atatcctgac 480  
ttattcgagt ggttttgtgt gaagacactg aaagtgtgct gctctccagg aacctacggc 540  
cccgactgtc tcgcatgcca gggcgggatcc cagagggcct gcagcgggaa tggccactgc 600  
agcggagatg ggagcagaca gggcgacggg tcctgcccgt gccacatggg gtaccagggc 660

```

ccgctgtgca ctgactgcat ggacggctac ttcagctcgc tccggaacga gaccacagc 720
atctgcacag cctgtgacga gtcctgcaag acgtgctcgg gcctgaccaa cagagactgc 780
ggcgagtgtg aagtgggctg ggtgctggac gagggcgcc gtgtggatgt ggacgagtgt 840
gcggccgagc cgcctccctg cagcgtcgcg cagttctgta agaacgcaa cggctcctac 900
acgtgcgaag agtgtgactc cagctgtgtg ggctgcacag gggaaggccc aggaaactgt 960
aaagagtgtg tctctggcta cgcgagggag cacggacagt gtgcagatgt ggacgagtgc 1020
tcactagcag aaaaaacctg tgtgaggaaa aacgaaaact gctacaatac tccagggagc 1080
tacgtctgtg tgtgtcctga cggcttcgaa gaaacggaag atgcctgtgt gccgccggca 1140
gaggtgaag ccacagaagg agaaagccc acacagctgc cctcccgcga agacctgtaa 1200
tgtgccggac ttacccttta aattattcag aaggatgtcc cgtggaaaat gtggccctga 1260
ggatgccgtc tcctgcagtg gacagcggcg gggagaggct gcctgctctc taacggttga 1320
ttctcatttg tcccttaaac agctgcattt cttggttgtt cttaaacaga cttgtatatt 1380
ttgatacagt tctttgtaat aaaattgacc attgtaggta atcaggagga aaaaaaaaaa 1440
aaaaaaaaaa aaagggcggc cgcgactcta gactcgacct gcagaagctt ggccgccatg 1500
gccaacttg tttattgcag cttataatgg ttacaaataa agcaatagca tcacaaattt 1560
cacaaataaa gcattttttt cactgcattc tagttgtggt ttgtccaaac tcatcaatgt 1620
atcttatcat gtctggatcg ggaattaatt cggcgcagca ccatggcctg aaataacctc 1680
tgaaagagga acttggttag gtaccttctg aggcggaaag aaccagctgt ggaatgtgtg 1740
tcagttaggg tgtggaaagt cccaggctc cccagcaggc agaagtatgc aagcatgcat 1800
ctcaattagt cagcaacca gtttt 1825

```

```

<210> 2
<211> 353
<212> PRT
<213> Homo sapiens

```

```

<400> 2
Met Arg Leu Pro Arg Arg Ala Ala Leu Gly Leu Leu Pro Leu Leu Leu
  1              5              10              15

Leu Leu Pro Pro Ala Pro Glu Ala Ala Lys Lys Pro Thr Pro Cys His
      20              25              30

Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
      35              40              45

Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
      50              55              60

Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
      65              70              75              80

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
      85              90              95

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
      100              105              110

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
      115              120              125

Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
      130              135              140

```

CCGCTGTGCA CTGACTGCAT GGACGGCTAC TTCAGCTCGC TCCGGAACGA GACCACAGC 720

Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg  
 145 150 155 160  
 Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu  
 165 170 175  
 Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr  
 180 185 190  
 His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
 195 200 205  
 Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp  
 210 215 220  
 Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro  
 225 230 235 240  
 Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys  
 245 250 255  
 Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly  
 260 265 270  
 Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys  
 275 280 285  
 Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys  
 290 295 300  
 Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro  
 305 310 315 320  
 Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala  
 325 330 335  
 Glu Ala Thr Glu Gly Glu Ser Pro Thr Gln Leu Pro Ser Arg Glu Asp  
 340 345 350  
 Leu

<210> 3  
 <211> 2206  
 <212> DNA  
 <213> Homo sapiens

<400> 3  
 caggccaac tgcacctcg ttctatcgat tgaattcccc ggggatacctc tagagatccc 60  
 tcgacctcga cccacgcgtc cgccaggccg ggaggcgacg cgcccagccg tctaaacggg 120  
 aacagccctg gctgagggag ctgcagcgca gcagagtatc tgacggcgcc aggttgcgta 180  
 ggtgcggcac gaggagtttt cccggcagcg aggaggtcct gagcagcatg gcccgaggaga 240



```
<210> 4
<211> 379
<212> PRT
<213> Homo sapiens
```

Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp Ser  
1 5 10 15

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu  
35 40 45

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

65					70						75				80
Pro	Val	Asn	Ile	His	Ser	Met	Asn	Phe	Thr	Trp	Gln	Ala	Ala	Gly	Gln
				85					90					95	
Ala	Glu	Tyr	Phe	Tyr	Glu	Phe	Leu	Ser	Leu	Arg	Ser	Leu	Asp	Lys	Gly
			100					105					110		
Ile	Met	Ala	Asp	Pro	Thr	Val	Asn	Val	Pro	Leu	Leu	Gly	Thr	Val	Pro
		115					120					125			
His	Lys	Ala	Ser	Val	Val	Gln	Val	Gly	Phe	Pro	Cys	Leu	Gly	Lys	Gln
	130					135					140				
Asp	Gly	Val	Ala	Ala	Phe	Glu	Val	Asp	Val	Ile	Val	Met	Asn	Ser	Glu
145					150					155					160
Gly	Asn	Thr	Ile	Leu	Gln	Thr	Pro	Gln	Asn	Ala	Ile	Phe	Phe	Lys	Thr
				165					170					175	
Cys	Gln	Gln	Ala	Glu	Cys	Pro	Gly	Gly	Cys	Arg	Asn	Gly	Gly	Phe	Cys
			180					185					190		
Asn	Glu	Arg	Arg	Ile	Cys	Glu	Cys	Pro	Asp	Gly	Phe	His	Gly	Pro	His
		195					200					205			
Cys	Glu	Lys	Ala	Leu	Cys	Thr	Pro	Arg	Cys	Met	Asn	Gly	Gly	Leu	Cys
	210					215					220				
Val	Thr	Pro	Gly	Phe	Cys	Ile	Cys	Pro	Pro	Gly	Phe	Tyr	Gly	Val	Asn
225					230					235					240
Cys	Asp	Lys	Ala	Asn	Cys	Ser	Thr	Thr	Cys	Phe	Asn	Gly	Gly	Thr	Cys
				245					250					255	
Phe	Tyr	Pro	Gly	Lys	Cys	Ile	Cys	Pro	Pro	Gly	Leu	Glu	Gly	Glu	Gln
			260					265					270		
Cys	Glu	Ile	Ser	Lys	Cys	Pro	Gln	Pro	Cys	Arg	Asn	Gly	Gly	Lys	Cys
		275					280					285			
Ile	Gly	Lys	Ser	Lys	Cys	Lys	Cys	Ser	Lys	Gly	Tyr	Gln	Gly	Asp	Leu
	290					295					300				
Cys	Ser	Lys	Pro	Val	Cys	Glu	Pro	Gly	Cys	Gly	Ala	His	Gly	Thr	Cys
305					310					315					320
His	Glu	Pro	Asn	Lys	Cys	Gln	Cys	Gln	Glu	Gly	Trp	His	Gly	Arg	His
				325					330					335	
Cys	Asn	Lys	Arg	Tyr	Glu	Ala	Ser	Leu	Ile	His	Ala	Leu	Arg	Pro	Ala
			340					345					350		

10420335640660

Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu  
 355 360 365

Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp  
 370 375

<210> 5  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 5  
 agggagcaccg gacagtgtgc agatgtggac gagtgtcac tagca 45

<210> 6  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 6  
 agagtgtatc tctggctacg c 21

<210> 7  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 7  
 taagtccggc acattacagg tc 22

<210> 8  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 8  
 cccacgatgt atgaatggtg gacttttgtg gactcctggt ttctgcac 49

PH20-0361060

<210> 9  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 9  
 aaagacgcat ctgcgagtgt cc 22

<210> 10  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 10  
 tgctgatttc acactgctct ccc 23

<210> 11  
 <211> 2197  
 <212> DNA  
 <213> Homo sapiens

<400> 11  
 cggacgcgtg ggcgtccggc ggtcgcagag ccaggaggcg gaggcgcgcg ggccagcctg 60  
 ggccccagcc cacaccttca ccaggggcca ggagccacca tgtggcgatg tccactgggg 120  
 ctactgctgt tgctgccgct ggctggccac ttggctcttg gtgccagca gggctcgtggg 180  
 cgccgggagc tagcaccggg tctgcacctg cggggcatcc gggacgcggg aggccgggtac 240  
 tgccaggagc aggacctgtg ctgccgcggc cgtgccgacg actgtgccct gccctacctg 300  
 ggcgccatct gttactgtga cctcttctgc aaccgcacgg tctccgactg ctgccctgac 360  
 ttctgggact tctgcctcgg cgtgccaccc ccttttcccc cgatccaagg atgtatgcat 420  
 ggaggtcgta tctatccagt cttgggaacg tactgggaca actgtaaccg ttgcacctgc 480  
 caggagaaca ggcagtggca tgggtgatcc agacatgac aaagccatca accagggcaa 540  
 ctatggctgg caggctggga accacagcgc cttctggggc atgaccctgg atgagggcac 600  
 tcgtaccgc ctgggcacca tccgcccatc ttcctcggtc atgaacatgc atgaaattta 660  
 tacagtgtg aaccagggg aggtgcttcc cacagccttc gaggcctctg agaagtggcc 720  
 caacctgatt catgagcctc ttgaccaagg caactgtgca ggctcctggg ccttctccac 780  
 agcagctgtg gcatccgatc gtgtctcaat ccattctctg ggacacatga cgctgtcct 840  
 gtcgccccag aacctgctgt cttgtgacac ccaccagcag cagggtgcc gcggtgggcg 900  
 tctcgatggt gcctggtggt tctgcgtcg ccgaggggtg gtgtctgacc actgctaccc 960  
 cttctcgggc cgtgaacgag acgaggctgg ccctgcgcc ccctgtatga tgcacagccg 1020  
 agccatgggt cggggcaagc gccaggccac tgcccactgc cccaacagct atgttaataa 1080  
 caatgacatc taccaggtca ctctgtcta ccgcctcggc tccaacgaca aggagatcat 1140  
 gaaggagctg atggagaatg gccctgtcca agccctcatg gaggtgcatg aggacttctt 1200  
 cctatacaag ggaggcatct acagccacac gccagtgagc cttgggaggc cagagagata 1260  
 ccgccggcat gggacccact cagtcaagat cacaggatgg ggagaggaga cgctgccaga 1320

tggaggacg ctcaaatact ggactgcggc caactcctgg ggcccagcct ggggcgagag 1380  
 gggccacttc cgcacgtgc gcggcgtaa tgagtgcgac atcgagagct tcgtgctggg 1440  
 cgtctggggc cgcgtgggca tggaggacat gggtcatcac tgaggctgcg ggcaccacgc 1500  
 ggggtccggc ctgggatcca ggctaagggc cggcggaaga ggcccgaatg gggcggtgac 1560  
 cccagcctcg cccgacagag cccggggcgc aggcgggcgc cagggcgcta atcccggcg 1620  
 gggttccgct gacgcagcgc cccgcctggg agccgcgggc aggcgagact ggcggagccc 1680  
 ccagacctcc cagtggggac ggggcagggc ctggcctggg aagagcacag ctgcagatcc 1740  
 caggcctctg gcgccccac tcaagactac caaagccagg acacctcaag tctccagccc 1800  
 caatacccca cccaatccc gtattctttt tttttttt ttagacaggg tcttgcctcg 1860  
 ttgcccaggt tggagtgcag tggcccatca gggctcactg taacctccga ctctggggtt 1920  
 caagtgacct tcccacctca gcctctcaag tagctgggac tacagggtgca ccaccacacc 1980  
 tggctaattt ttgtattttt tgtaaagagg ggggtctcac tgtgttgccc aggctgggtt 2040  
 cgaactcctg ggctcaagcg gtccacctgc ctccgcctcc caaagtgtcg ggattgcagg 2100  
 catgagccac tgcacccagc cctgtattct tattcttcag atattttatt ttcttttcac 2160  
 tgttttaaaa taaaaccaa gtattgataa aaaaaa 2197

<210> 12

<211> 164

<212> PRT

<213> Homo sapiens

<400> 12

Met Trp Arg Cys Pro Leu Gly Leu Leu Leu Leu Pro Leu Ala Gly  
 1 5 10 15  
 His Leu Ala Leu Gly Ala Gln Gln Gly Arg Gly Arg Arg Glu Leu Ala  
 20 25 30  
 Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys  
 35 40 45  
 Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu  
 50 55 60  
 Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr  
 65 70 75 80  
 Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro  
 85 90 95  
 Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr  
 100 105 110  
 Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln  
 115 120 125  
 Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln  
 130 135 140  
 Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly  
 145 150 155 160  
 His Asp Pro Gly

101120" 99040600



ttcgaaggcct ctgagaagtg gccc

24

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 15

ggcggatatct ctctggcctc cc

22

<210> 16

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 16

ttctccacag cagctgtggc atccgatcgt gtctcaatcc attctctggg

50

<210> 17

<211> 960

<212> DNA

<213> Homo sapiens

<400> 17

gctgcttgcc ctgttgatgg caggcttggc cctgcagcca ggcaactgcc tgctgtgcta 60  
ctcctgcaaa gcccaggtga gcaacgagga ctgcctgcag gtggagaact gcaccagct 120  
gggggagcag tgctggaccg cgcgcatccg cgcagttggc ctctgaccg tcatcagcaa 180  
aggetgcagc ttgaactgcg tggatgactc acaggactac tacgtgggca agaagaacat 240  
cacgtgctgt gacaccgact tgtgcaacgc cagcggggcc catgccctgc agccggctgc 300  
cgccatcctt gcgtgctcc ctgcactcgg cctgctgctc tggggacccg gccagctata 360  
ggctctgggg ggccccgctg cagcccacac tgggtgtggt gccccaggcc tctgtgccac 420  
tcttcacaga cctggcccag tgggagcctg tcttggttcc tgaggcacat cctaacgcaa 480  
gtctgaccat gtatgtctgc acccctgtcc cccaccctga ccctcccatg gccctctcca 540  
ggactcccac ccggcagatc agctctagtg acacagatcc gcctgcagat ggcccccca 600  
accctctctg ctgctgtttc catggcccag cattctccac ccttaaccct gtgctcaggc 660  
acctcttccc ccaggaagcc ttcctgccc acccatcta tgacttgagc caggtctggt 720  
ccgtggtgtc ccccgacccc agcaggggac aggcactcag gagggcccag taaaggctga 780  
gatgaagtgg actgagtaga actggaggac aagagtcgac gtgagttcct gggagtctcc 840  
agagatgggg cctggaggcc tggaggaagg ggccaggcct cacattcgtg gggctccctg 900  
aatggcagcc tgagcacago gtaggcctt aataaacacc tgttggataa gccaaaaaaa 960

<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

TTTCTCAGCTGTGGC





[illegible]

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

24

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

44

<213> Homo sapiens

ccccgcgctc	cgaacctctc	cagcgatggg	agccgcccgc	ctgctgccca	acctactctc	60
gtgcttacag	ctgctgattc	tctgctgtca	aactcagtac	gtgagggacc	agggcgccat	120
gaccgaccag	ctgagcaggc	ggcagatccg	cgagtaccaa	ctctacagca	ggaccagtgg	180
caagcacgtg	caggtcaccg	ggcgctcgcat	ctccgccacc	gccgaggacg	gcaacaagtt	240
tgccaagctc	atagtggaga	cggacacggt	tggcagccgg	gttcgcattc	aaggggctga	300
gagtgagaag	tacatctgta	tgaacaagag	gggcaagctc	atcggaagc	ccagcgggaa	360
gagcaaagac	tgcgtgttca	cggagatcgt	gctggagaac	aactatacgg	ccttcagaa	420
cgccgggcac	gagggctggt	tcatggcctt	cacgcggcag	gggcggcccc	gccaggcttc	480
cccgagccgc	cagaaccagc	gcgaggccca	cttcataaag	cgctctacc	aaggccagct	540
gcccttcccc	aaccacgccg	agaagcagaa	gcagttcgag	tttgtgggct	ccgccccac	600
ccgcgggacc	aagcgcacac	ggcgccccca	gcccctcacg	tagtctggga	ggcagggggc	660
agcagccctt	gggcgccttc	cccacccctt	tcccttctta	atccaaggac	tgggctgggg	720
tggcgggagg	ggagccagat	ccccgaggga	ggaccctgag	ggccgcgaag	catccgagcc	780
cccagctggg	aaggggcagg	ccggtgcccc	aggggcggct	ggcacagtgc	ccccttcccg	840
gacgggtggc	aggccctgga	gaggaactga	gtgtcaccct	gatctcaggc	caccagcctc	900
tgccggcctc	ccagccgggc	tctgaagcc	cgctgaaagg	tcagcgactg	aaggccttgc	960
agacaaccgt	ctggcaggtg	ctgtcctcaa	aatctgcttc	tcggattctc	ctcagctctc	1020
ccccagcccc	caaactcctc	ctggtctagac	tgtaggaagg	gacttttgtt	tgtttgtttg	1080
tttcaggaaa	aaagaaaagg	agagagagga	aaatagaggg	tgtgtccactc	ctcacattcc	1140
acgaccccaq	cctgcacccc	accccccaact	cccaqccccq	qaataaaaacc	attttctctc	1200

<213> Homo sapiens

&lt;400&gt; 23

Met	Gly	Ala	Ala	Arg	Leu	Leu	Pro	Asn	Leu	Thr	Leu	Cys	Leu	Gln	Leu
1				5					10					15	

Leu	Ile	Leu	Cys	Cys	Gln	Thr	Gln	Tyr	Val	Arg	Asp	Gln	Gly	Ala	Met
			20					25					30		

Thr	Asp	Gln	Leu	Ser	Arg	Arg	Gln	Ile	Arg	Glu	Tyr	Gln	Leu	Tyr	Ser
	35						40					45			

Arg	Thr	Ser	Gly	Lys	His	Val	Gln	Val	Thr	Gly	Arg	Arg	Ile	Ser	Ala
	50					55					60				

Thr	Ala	Glu	Asp	Gly	Asn	Lys	Phe	Ala	Lys	Leu	Ile	Val	Glu	Thr	Asp
65					70					75					80

Thr	Phe	Gly	Ser	Arg	Val	Arg	Ile	Lys	Gly	Ala	Glu	Ser	Glu	Lys	Tyr
				85					90					95	

Ile	Cys	Met	Asn	Lys	Arg	Gly	Lys	Leu	Ile	Gly	Lys	Pro	Ser	Gly	Lys
			100					105					110		

Ser	Lys	Asp	Cys	Val	Phe	Thr	Glu	Ile	Val	Leu	Glu	Asn	Asn	Tyr	Thr
		115					120					125			

Ala	Phe	Gln	Asn	Ala	Arg	His	Glu	Gly	Trp	Phe	Met	Ala	Phe	Thr	Arg
	130					135					140				

Gln	Gly	Arg	Pro	Arg	Gln	Ala	Ser	Arg	Ser	Arg	Gln	Asn	Gln	Arg	Glu
145					150					155					160

Ala	His	Phe	Ile	Lys	Arg	Leu	Tyr	Gln	Gly	Gln	Leu	Pro	Phe	Pro	Asn
				165					170					175	

His	Ala	Glu	Lys	Gln	Lys	Gln	Phe	Glu	Phe	Val	Gly	Ser	Ala	Pro	Thr
			180					185					190		

Arg	Arg	Thr	Lys	Arg	Thr	Arg	Arg	Pro	Gln	Pro	Leu	Thr
		195					200				205	

&lt;210&gt; 24

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic oligonucleotide probe

&lt;400&gt; 24

cagtacgtga gggaccaggg cgccatga

28

&lt;210&gt; 25

1  
 2  
 3  
 4  
 5  
 6  
 7  
 8  
 9  
 10  
 11  
 12  
 13  
 14  
 15  
 16  
 17  
 18  
 19  
 20  
 21  
 22  
 23  
 24  
 25  
 26  
 27  
 28  
 29  
 30  
 31  
 32  
 33  
 34  
 35  
 36  
 37  
 38  
 39  
 40  
 41  
 42  
 43  
 44  
 45  
 46  
 47  
 48  
 49  
 50  
 51  
 52  
 53  
 54  
 55  
 56  
 57  
 58  
 59  
 60  
 61  
 62  
 63  
 64  
 65  
 66  
 67  
 68  
 69  
 70  
 71  
 72  
 73  
 74  
 75  
 76  
 77  
 78  
 79  
 80  
 81  
 82  
 83  
 84  
 85  
 86  
 87  
 88  
 89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100  
 101  
 102  
 103  
 104  
 105  
 106  
 107  
 108  
 109  
 110  
 111  
 112  
 113  
 114  
 115  
 116  
 117  
 118  
 119  
 120  
 121  
 122  
 123  
 124  
 125  
 126  
 127  
 128  
 129  
 130  
 131  
 132  
 133  
 134  
 135  
 136  
 137  
 138  
 139  
 140  
 141  
 142  
 143  
 144  
 145  
 146  
 147  
 148  
 149  
 150  
 151  
 152  
 153  
 154  
 155  
 156  
 157  
 158  
 159  
 160  
 161  
 162  
 163  
 164  
 165  
 166  
 167  
 168  
 169  
 170  
 171  
 172  
 173  
 174  
 175  
 176  
 177  
 178  
 179  
 180  
 181  
 182  
 183  
 184  
 185  
 186  
 187  
 188  
 189  
 190  
 191  
 192  
 193  
 194  
 195  
 196  
 197  
 198  
 199  
 200  
 201  
 202  
 203  
 204  
 205  
 206  
 207  
 208  
 209  
 210  
 211  
 212  
 213  
 214  
 215  
 216  
 217  
 218  
 219  
 220  
 221  
 222  
 223  
 224  
 225  
 226  
 227  
 228  
 229  
 230  
 231  
 232  
 233  
 234  
 235  
 236  
 237  
 238  
 239  
 240  
 241  
 242  
 243  
 244  
 245  
 246  
 247  
 248  
 249  
 250  
 251  
 252  
 253  
 254  
 255  
 256  
 257  
 258  
 259  
 260  
 261  
 262  
 263  
 264  
 265  
 266  
 267  
 268  
 269  
 270  
 271  
 272  
 273  
 274  
 275  
 276  
 277  
 278  
 279  
 280  
 281  
 282  
 283  
 284  
 285  
 286  
 287  
 288  
 289  
 290  
 291  
 292  
 293  
 294  
 295  
 296  
 297  
 298  
 299  
 300  
 301  
 302  
 303  
 304  
 305  
 306  
 307  
 308  
 309  
 310  
 311  
 312  
 313  
 314  
 315  
 316  
 317  
 318  
 319  
 320  
 321  
 322  
 323  
 324  
 325  
 326  
 327  
 328  
 329  
 330  
 331  
 332  
 333  
 334  
 335  
 336  
 337  
 338  
 339  
 340  
 341  
 342  
 343  
 344  
 345  
 346  
 347  
 348  
 349  
 350  
 351  
 352  
 353  
 354  
 355  
 356  
 357  
 358  
 359  
 360  
 361  
 362  
 363  
 364  
 365  
 366  
 367  
 368  
 369  
 370  
 371  
 372  
 373  
 374  
 375  
 376  
 377  
 378  
 379  
 380  
 381  
 382  
 383  
 384  
 385  
 386  
 387  
 388  
 389  
 390  
 391  
 392  
 393  
 394  
 395  
 396  
 397  
 398  
 399  
 400  
 401  
 402  
 403  
 404  
 405  
 406  
 407  
 408  
 409  
 410  
 411  
 412  
 413  
 414  
 415  
 416  
 417  
 418  
 419  
 420  
 421  
 422  
 423  
 424  
 425  
 426  
 427  
 428  
 429  
 430  
 431  
 432  
 433  
 434  
 435  
 436  
 437  
 438  
 439  
 440  
 441  
 442  
 443  
 444  
 445  
 446  
 447  
 448  
 449  
 450  
 451  
 452  
 453  
 454  
 455  
 456  
 457  
 458  
 459  
 460  
 461  
 462  
 463  
 464  
 465  
 466  
 467  
 468  
 469  
 470  
 471  
 472  
 473  
 474  
 475  
 476  
 477  
 478  
 479  
 480  
 481  
 482  
 483  
 484  
 485  
 486  
 487  
 488  
 489  
 490  
 491  
 492  
 493  
 494  
 495  
 496  
 497  
 498  
 499  
 500  
 501  
 502  
 503  
 504  
 505  
 506  
 507  
 508  
 509  
 510  
 511  
 512  
 513  
 514  
 515  
 516  
 517  
 518  
 519  
 520  
 521  
 522  
 523  
 524  
 525  
 526  
 527  
 528  
 529  
 530  
 531  
 532  
 533  
 534  
 535  
 536  
 537  
 538  
 539  
 540  
 541  
 542  
 543  
 544  
 545  
 546  
 547  
 548  
 549  
 550  
 551  
 552  
 553  
 554  
 555  
 556  
 557  
 558  
 559  
 560  
 561  
 562  
 563  
 564  
 565  
 566  
 567  
 568  
 569  
 570  
 571  
 572  
 573  
 574  
 575  
 576  
 577  
 578  
 579  
 580  
 581  
 582  
 583  
 584  
 585  
 586  
 587  
 588  
 589  
 590  
 591  
 592  
 593  
 594  
 595  
 596  
 597  
 598  
 599  
 600  
 601  
 602  
 603  
 604  
 605  
 606  
 607  
 608  
 609  
 610  
 611  
 612  
 613  
 614  
 615  
 616  
 617  
 618  
 619  
 620  
 621  
 622  
 623  
 624  
 625  
 626  
 627  
 628  
 629  
 630  
 631  
 632  
 633  
 634  
 635  
 636  
 637  
 638  
 639  
 640  
 641  
 642  
 643  
 644  
 645  
 646  
 647  
 648  
 649  
 650  
 651  
 652  
 653  
 654  
 655  
 656  
 657  
 658  
 659  
 660  
 661  
 662  
 663  
 664  
 665  
 666  
 667  
 668  
 669  
 670  
 671  
 672  
 673  
 674  
 675  
 676  
 677  
 678  
 679  
 680  
 681  
 682  
 683  
 684  
 685  
 686  
 687  
 688  
 689  
 690  
 691  
 692  
 693  
 694  
 695  
 696  
 697  
 698  
 699  
 700  
 701  
 702  
 703  
 704  
 705  
 706  
 707  
 708  
 709  
 710  
 711  
 712  
 713  
 714  
 715  
 716  
 717  
 718  
 719  
 720  
 721  
 722  
 723  
 724  
 725  
 726  
 727  
 728  
 729  
 730  
 731  
 732  
 733  
 734  
 735  
 736  
 737  
 738  
 739  
 740  
 741  
 742  
 743  
 744  
 745  
 746  
 747  
 748  
 749  
 750  
 751  
 752  
 753  
 754  
 755  
 756  
 757  
 758  
 759  
 760  
 761  
 762  
 763  
 764  
 765  
 766  
 767  
 768  
 769  
 770  
 771  
 772  
 773  
 774  
 775  
 776  
 777  
 778  
 779  
 780  
 781  
 782  
 783  
 784  
 785  
 786  
 787  
 788  
 789  
 790  
 791  
 792  
 793  
 794  
 795  
 796  
 797  
 798  
 799  
 800  
 801  
 802  
 803  
 804  
 805  
 806  
 807  
 808  
 809  
 810  
 811  
 812  
 813  
 814  
 815  
 816  
 817  
 818  
 819  
 820  
 821  
 822  
 823  
 824  
 825  
 826  
 827  
 828  
 829  
 830  
 831  
 832  
 833  
 834  
 835  
 836  
 837  
 838  
 839  
 840  
 841  
 842  
 843  
 844  
 845  
 846  
 847  
 848  
 849  
 850  
 851  
 852  
 853  
 854  
 855  
 856  
 857  
 858  
 859  
 860  
 861  
 862  
 863  
 864  
 865  
 866  
 867  
 868  
 869  
 870  
 871  
 872  
 873  
 874  
 875  
 876  
 877  
 878  
 879  
 880  
 881  
 882  
 883  
 884  
 885  
 886  
 887  
 888  
 889  
 890  
 891  
 892  
 893  
 894  
 895  
 896  
 897  
 898  
 899  
 900  
 901  
 902  
 903  
 904  
 905  
 906  
 907  
 908  
 909  
 910  
 911  
 912  
 913  
 914  
 915  
 916  
 917  
 918  
 919  
 920  
 921  
 922  
 923  
 924  
 925  
 926  
 927  
 928  
 929  
 930  
 931  
 932  
 933  
 934  
 935  
 936  
 937  
 938  
 939  
 940  
 941  
 942  
 943  
 944  
 945  
 946  
 947  
 948  
 949  
 950  
 951  
 952  
 953  
 954  
 955  
 956  
 957  
 958  
 959  
 960  
 961  
 962  
 963  
 964  
 965  
 966  
 967  
 968  
 969  
 970  
 971  
 972  
 973  
 974  
 975  
 976  
 977  
 978  
 979  
 980  
 981  
 982  
 983  
 984  
 985  
 986  
 987  
 988  
 989  
 990  
 991  
 992  
 993  
 994  
 995  
 996  
 997  
 998  
 999  
 1000

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 25  
 ccggtgacct gcacgtgctt gccca 24

<210> 26  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<220>  
 <221> modified\_base  
 <222> (21)  
 <223> a, t, c or g

<400> 26  
 gcggatctgc cgectgctca nctggctcgg catggcgccc t 41

<210> 27  
 <211> 2479  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
 acttgccatc acctggtgcc agtgtggaaa aattctccct gttgaatttt ttgcacatgg 60  
 aggacagcag caaagagggc aacacaggct gataagacca gagacagcag ggagattatt 120  
 ttaccatacg cctcaggac gtccctctta gctggagttc tggacttcaa cagaacccca 180  
 tccagtcatt ttgattttgc tgtttatttt ttttttcttt ttctttttcc caccacattg 240  
 tatttttatt ccgtacttca gaaatgggccc tacagaccac aaagtggccc agccatgggg 300  
 cttttttcct gaagtcttgg cttatcattt ccctggggct ctactcacag gtgtccaaac 360  
 tcctggcctg ccctagtgtg tgccgctgcg acaggaactt tgtctactgt aatgagcgaa 420  
 gcttgacctc agtgcctctt gggatcccgg agggcgtaac cgtactctac ctccacaaca 480  
 accaaattaa taatgctgga tttcctgcag aactgcacaa tgtacagtcg gtgcacacgg 540  
 tctacctgta tggcaaccaa ctggacgaat tccccatgaa ctttcccaag aatgtcagag 600  
 ttctccattt gcaggaaaac aatattcaga ccatttcacg ggctgctctt gccagctct 660  
 tgaagcttga agagctgcac ctggatgaca actccatata cacagtgggg gtggaagacg 720  
 gggccttccg ggaggctatt agcctcaaat tgttgttttt gtctaagaat cacctgagca 780  
 gtgtgcctgt tgggcttccct gtggacttgc aagagctgag agtggatgaa aatcgaattg 840  
 ctgtcatatc cgacatggcc ttccagaatc tcacgagctt ggagcgtctt attgtggacg 900  
 ggaacctcct gaccaacaag ggtatcgccg agggcacctt cagccatctc accaagctca 960  
 aggaattttc aattgtacgt aattcgctgt cccaccctcc tcccgatctc ccaggtagcg 1020  
 atctgatcag gctctatttg caggacaacc agataaacca cattcctttg acagccttct 1080  
 caaatctgcg taagctggaa cggctggata tatccaacaa ccaactgcgg atgctgactc 1140

aagggggtttt tgataatctc tccaacctga agcagctcac tgctcggaat aacccttggt 1200  
tttgtgactg cagtattaaa tgggtcacag aatgggtcaa atatatccct tcatctctca 1260  
acgtgcgggg tttcatgtgc caaggctctg aacaagtccg ggggatggcc gtcagggaat 1320  
taaatatgaa tcttttgtcc tgtcccacca cgaccccccg cctgcctctc ttcaccccag 1380  
ccccaagtac agcttctccg accactcagc ctcccaccct ctctattcca aaccctagca 1440  
gaagctacac gcttccaact cctaccacat cgaaacttcc cacgattcct gactgggatg 1500  
gcagagaaaag agtgacccca cctatttctg aacggatcca gctctctatc cattttgtga 1560  
atgatacttc cattcaagtc agctggctct ctctcttcac cgtgatggca tacaaactca 1620  
catgggtgaa aatggggccac agttagtag ggggcatcgt tcaggagcgc atagtcagcg 1680  
gtgagaagca acacctgagc ctggttaact tagagccccg atccacctat cggatttggt 1740  
tagtgccact ggatgctttt aactaccgcg cggtagaaga caccatttgt tcagaggcca 1800  
ccacccatgc ctctatctg aacaacggca gcaacacagc gtccagccat gagcagacga 1860  
cgtcccacag catgggctcc ccctttctgc tggcgggctt gatcgggggc gcggtgatat 1920  
ttgtgctggt ggtcttctc agcgtctttt gctggcatat gcacaaaaag gggcgctaca 1980  
cctcccagaa gtggaaatac aaccggggcc ggcggaaaga tgattattgc gaggcaggca 2040  
ccaagaagga caactccatc ctggagatga cagaaaccag ttttcagatc gtctccttaa 2100  
ataacgatca actccttaa ggagatttca gactgcagcc catttacacc ccaaaggggg 2160  
gcattaatta cacagactgc catatcccca acaacatgcg atactgcaac agcagcgtgc 2220  
cagacctgga gcaactgcat acgtgacagc cagaggccca gcgttatcaa ggcggacaat 2280  
tagactcttg agaacacact cgtgtgtgca cataaagaca cgcagattac atttgataaa 2340  
tgttacacag atgcatttgt gcatttgaat actctgtaat ttatacgggtg tactatataa 2400  
tgggatttaa aaaaagtgt atcttttcta tttcaagtta attacaaaca gttttgtaac 2460  
tctttgcttt ttaaattctt 2479

<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

Met	Gly	Leu	Gln	Thr	Thr	Lys	Trp	Pro	Ser	His	Gly	Ala	Phe	Phe	Leu
1				5				10					15		
Lys	Ser	Trp	Leu	Ile	Ile	Ser	Leu	Gly	Leu	Tyr	Ser	Gln	Val	Ser	Lys
			20					25					30		
Leu	Leu	Ala	Cys	Pro	Ser	Val	Cys	Arg	Cys	Asp	Arg	Asn	Phe	Val	Tyr
		35					40					45			
Cys	Asn	Glu	Arg	Ser	Leu	Thr	Ser	Val	Pro	Leu	Gly	Ile	Pro	Glu	Gly
	50					55					60				
Val	Thr	Val	Leu	Tyr	Leu	His	Asn	Asn	Gln	Ile	Asn	Asn	Ala	Gly	Phe
	65				70					75				80	
Pro	Ala	Glu	Leu	His	Asn	Val	Gln	Ser	Val	His	Thr	Val	Tyr	Leu	Tyr
				85					90					95	
Gly	Asn	Gln	Leu	Asp	Glu	Phe	Pro	Met	Asn	Leu	Pro	Lys	Asn	Val	Arg
			100					105					110		
Val	Leu	His	Leu	Gln	Glu	Asn	Asn	Ile	Gln	Thr	Ile	Ser	Arg	Ala	Ala
		115					120					125			

004420-9540660

Leu	Ala	Gln	Leu	Leu	Lys	Leu	Glu	Glu	Leu	His	Leu	Asp	Asp	Asn	Ser
130						135					140				
Ile	Ser	Thr	Val	Gly	Val	Glu	Asp	Gly	Ala	Phe	Arg	Glu	Ala	Ile	Ser
145					150					155				160	
Leu	Lys	Leu	Leu	Phe	Leu	Ser	Lys	Asn	His	Leu	Ser	Ser	Val	Pro	Val
				165					170					175	
Gly	Leu	Pro	Val	Asp	Leu	Gln	Glu	Leu	Arg	Val	Asp	Glu	Asn	Arg	Ile
			180					185					190		
Ala	Val	Ile	Ser	Asp	Met	Ala	Phe	Gln	Asn	Leu	Thr	Ser	Leu	Glu	Arg
		195					200					205			
Leu	Ile	Val	Asp	Gly	Asn	Leu	Leu	Thr	Asn	Lys	Gly	Ile	Ala	Glu	Gly
210					215					220					
Thr	Phe	Ser	His	Leu	Thr	Lys	Leu	Lys	Glu	Phe	Ser	Ile	Val	Arg	Asn
225					230					235				240	
Ser	Leu	Ser	His	Pro	Pro	Pro	Asp	Leu	Pro	Gly	Thr	His	Leu	Ile	Arg
				245					250					255	
Leu	Tyr	Leu	Gln	Asp	Asn	Gln	Ile	Asn	His	Ile	Pro	Leu	Thr	Ala	Phe
			260					265					270		
Ser	Asn	Leu	Arg	Lys	Leu	Glu	Arg	Leu	Asp	Ile	Ser	Asn	Asn	Gln	Leu
		275					280					285			
Arg	Met	Leu	Thr	Gln	Gly	Val	Phe	Asp	Asn	Leu	Ser	Asn	Leu	Lys	Gln
290					295					300					
Leu	Thr	Ala	Arg	Asn	Asn	Pro	Trp	Phe	Cys	Asp	Cys	Ser	Ile	Lys	Trp
305					310					315				320	
Val	Thr	Glu	Trp	Leu	Lys	Tyr	Ile	Pro	Ser	Ser	Leu	Asn	Val	Arg	Gly
				325					330					335	
Phe	Met	Cys	Gln	Gly	Pro	Glu	Gln	Val	Arg	Gly	Met	Ala	Val	Arg	Glu
			340					345					350		
Leu	Asn	Met	Asn	Leu	Leu	Ser	Cys	Pro	Thr	Thr	Thr	Pro	Gly	Leu	Pro
		355					360					365			
Leu	Phe	Thr	Pro	Ala	Pro	Ser	Thr	Ala	Ser	Pro	Thr	Thr	Gln	Pro	Pro
370						375					380				
Thr	Leu	Ser	Ile	Pro	Asn	Pro	Ser	Arg	Ser	Tyr	Thr	Pro	Pro	Thr	Pro
385					390					395				400	
Thr	Thr	Ser	Lys	Leu	Pro	Thr	Ile	Pro	Asp	Trp	Asp	Gly	Arg	Glu	Arg

415

<210>	29
<211>	21
<212>	DNA

10	100
15	150
20	200
25	250
30	300
35	350
40	400
45	450
50	500
55	550
60	600
65	650
70	700
75	750
80	800
85	850
90	900
95	950
100	1000
105	1050
110	1100
115	1150
120	1200
125	1250
130	1300
135	1350
140	1400
145	1450
150	1500
155	1550
160	1600
165	1650
170	1700
175	1750
180	1800
185	1850
190	1900
195	1950
200	2000
205	2050
210	2100
215	2150
220	2200
225	2250
230	2300
235	2350
240	2400
245	2450
250	2500
255	2550
260	2600
265	2650
270	2700
275	2750
280	2800
285	2850
290	2900
295	2950
300	3000
305	3050
310	3100
315	3150
320	3200
325	3250
330	3300
335	3350
340	3400
345	3450
350	3500
355	3550
360	3600
365	3650
370	3700
375	3750
380	3800
385	3850
390	3900
395	3950
400	4000
405	4050
410	4100
415	4150
420	4200
425	4250
430	4300
435	4350
440	4400
445	4450
450	4500
455	4550
460	4600
465	4650
470	4700
475	4750
480	4800
485	4850
490	4900
495	4950
500	5000
505	5050
510	5100
515	5150
520	5200
525	5250
530	5300
535	5350
540	5400
545	5450
550	5500
555	5550
560	5600
565	5650
570	5700
575	5750
580	5800
585	5850
590	5900
595	5950
600	6000
605	6050
610	6100
615	6150
620	6200
625	6250
630	6300
635	6350
640	6400
645	6450
650	6500
655	6550
660	6600
665	6650
670	6700
675	6750
680	6800
685	6850
690	6900
695	6950
700	7000
705	7050
710	7100
715	7150
720	7200
725	7250
730	7300
735	7350
740	7400
745	7450
750	7500
755	7550
760	7600
765	7650
770	7700
775	7750
780	7800
785	7850
790	7900
795	7950
800	8000
805	8050
810	8100
815	8150
820	8200
825	8250
830	8300
835	8350
840	8400
845	8450
850	8500
855	8550
860	8600
865	8650
870	8700
875	8750
880	8800
885	8850
890	8900
895	8950
900	9000
905	9050
910	9100
915	9150
920	9200
925	9250
930	9300
935	9350
940	9400
945	

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

cggctctacct gatatggcaac c

<210> 30

<212> DNA

<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

gcaggacaac cagataaacc ac

<210> 31

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

acgcagattt gagaaggctg tc

<210> 32

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac

<210> 33

<212> DNA

[illegible]

acttgagca agcggcggcg gcggagacag aggcagaggc agaagctggg gctccgtcct 60  
cgctcccac gacgatccc cgaggagagc cgcgccctc ggcgaggcga agaggccgac 120

gaggaagacc	cgggtggctg	cgccctgcc	tcgcttccca	ggcgccggcg	gctgcagcct	180
tgccctcctt	gctcgctctt	aaaatggaaa	agatgctcgc	aggctgcttt	ctgctgatcc	240
tcggacagat	cgctcctcct	cctgccgagg	ccagggagcg	gtcacgtggg	aggtccatct	300
ctaggggcag	acacgctcgg	accaccgcg	agacggccct	tctggagagt	tctgttgaga	360
acaagcgggc	agacctggtt	ttcatcattg	acagctctcg	cagtgtcaac	acccatgact	420
atgcaaaggt	caaggagttc	atcgtggaca	tcttgcaatt	cttggacatt	ggtcctgatg	480
tcacccgagt	gggctgctc	caatatggca	gcactgtcaa	gaatgagttc	tccctcaaga	540
ccttcaagag	gaagtccgag	gtggagcgtg	ctgtcaagag	gatgcggcat	ctgtccacgg	600
gcaccatgac	tgggctggcc	atccagtatg	ccctgaacat	cgcattctca	gaagcagagg	660
gggcccggcc	cctgaggggag	aatgtgccac	gggtcataat	gatcgtgaca	gatgggagac	720
ctcaggactc	cgtggccgag	gtggctgcta	aggcacggga	cacgggcac	ctaactcttg	780
ccattgggtg	gggccaggta	gacttcaaca	ccttgaagtc	cattgggagt	gagccctatg	840
aggaccatgt	cttccttggt	gccaatttca	gccagattga	gacgctgacc	tccgtgttcc	900
agaagaagtt	gtgcacggcc	cacatgtgca	gcacctgga	gcataactgt	gccactttct	960
gcatacaact	ccctgggtca	tacgtctgca	ggtgcaaaca	aggctacatt	ctcaactcgg	1020
atcagacgac	ttgcagaatc	caggatctgt	gtgccatgga	ggaccacaac	tgtgagcagc	1080
tctgtgtgaa	tgtgcggggc	tccttcgtct	gccagtgtca	cagtggctac	gccttggttg	1140
aggatgggaa	gaggtgtgtg	gctgtggact	actgtgcctc	agaaaaccac	ggatgtgaac	1200
atgagtgtgt	aaatgctgat	ggctcctacc	tttgccagtg	ccatgaagga	tttgccttta	1260
accagatga	aaaaacgtgc	acaaggatca	actactgtgc	actgaacaaa	ccgggctgtg	1320
agcatgagtg	cgtcaacatg	gaggagagct	actactgcgc	ctgccaccgt	ggctacactc	1380
tggaccccaa	tggcaaaacc	tgcagccgag	tggaccactg	tgcacagcag	gaccatggct	1440
gtgagcagct	gtgtctgaac	acggaggatt	ccttcgtctg	ccagtgtctc	gaaggcttcc	1500
tcatacaacg	ggacctcaag	acctgctccc	gggtggatta	ctgctgtctg	agtgacctg	1560
gttgtgaata	ctcctgtgtc	aacatggaca	gactctttgc	ctgtcagttg	cctgagggac	1620
acgtgctccg	cagcgatggg	aagacgtgtg	caaaattgga	ctcttgtgtc	ctgggggacc	1680
acggttgtga	acattcgtgt	gtaagcagtg	aagattcgtt	tgtgtgccag	tgctttgaag	1740
gttatatact	ccgtgaagat	ggaaaaacct	gcagaaggaa	agatgtctgc	caagctatag	1800
accatggctg	tgaacacatt	tgtgtgaaca	gtgacgactc	atacacgtgc	gagtgccttg	1860
agggattccg	gctcgctgag	gatgggaaac	gctgccgaag	gaaggatgtc	tgcaaatcaa	1920
cccaccatgg	ctgcgaacac	atttgtgtta	ataatgggaa	ttcctacatc	tgcaaatgct	1980
cagagggatt	tgttctagct	gaggagggaa	gacggtgcaa	gaaatgcact	gaaggcccaa	2040
ttgacctggg	ctttgtgata	gatggatcca	agagtcttgg	agaagagaat	tttgaggctg	2100
tgaagcagtt	tgtcactgga	attatagatt	ccttgacaat	ttcccccaa	gccgctcgag	2160
tggggctgct	ccagtattcc	acacaggtcc	acacagagtt	cactctgaga	aacttcaact	2220
cagccaaaga	catgaaaaaa	gccgtggccc	acatgaaata	catgggaaag	ggctctatga	2280
ctgggctggc	cctgaaacac	atgtttgaga	gaagttttac	ccaaggagaa	ggggccaggc	2340
ccctttccac	aagggtgccc	agagcagcca	ttgtgttcac	cgacggacgg	gctcaggatg	2400
acgtctccga	gtgggcccagt	aaagccaagg	ccaatggtat	cactatgtat	gctgttgggg	2460
taggaaaaagc	cattgaggag	gaactacaag	agattgcctc	tgagccca	aacaagcatc	2520
tcttctatgc	cgaagacttc	agcacaatgg	atgagataag	tgaaaaactc	aagaaaggca	2580
tctgtgaagc	tctagaagac	tccgatggaa	gacaggactc	tccagcaggg	gaactgccaa	2640
aaacgggtcca	acagccaaca	gaactctgagc	cagtcaccat	aaatatccaa	gacctacttt	2700
cctgtttctaa	ttttgcagtg	caacacagat	atctgtttga	agaagacaat	cttttacggg	2760
ctacacaaaa	gctttcccat	tcaacaaaac	cctcaggaag	ccctttggaa	gaaaaacacg	2820
atcaatgcaa	atgtgaaaac	cttataatgt	tccagaacct	tgcaaacgaa	gaagtaagaa	2880
aattaacaca	gcgcttagaa	gaaatgacac	agagaatgga	agcctctggaa	aatcgctga	2940
gatacagatg	aagattagaa	atcgcgacac	atttgtagtc	attgtatcac	ggattacaat	3000
gaacgcagtg	cagagcccca	aagctcaggc	tattgttaaa	tcaataatgt	tgtgaagtaa	3060
aacaatcagt	actgagaaac	ctggtttgcc	acagaacaaa	gacaagaagt	atacactaac	3120
ttgtataaat	ttatctagga	aaaaaatcct	tcagaattct	aagatgaatt	taccagggtga	3180
gaatgaataa	gctatgcaag	gtattttgtg	atatactgtg	gacacaactt	gcttctgcct	3240
catcctgcct	tagtgtgcaa	tctcatttga	ctatacgata	aagtttgcac	agtcttactt	3300



ctgtagaaca ctggccatag gaaatgctgt tttttgtac tggactttac cttgatatat 3360  
 gtatatggat gtatgcataa aatcatagga catatgtact tgtggaacaa gttggatttt 3420  
 ttatacaata ttaaaattca ccacttcag 3449

<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile  
 1 5 10 15  
 Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile  
 20 25 30  
 Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu  
 35 40 45  
 Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser  
 50 55 60  
 Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile  
 65 70 75 80  
 Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val  
 85 90 95  
 Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys  
 100 105 110  
 Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg  
 115 120 125  
 His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu  
 130 135 140  
 Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn  
 145 150 155 160  
 Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser  
 165 170 175  
 Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe  
 180 185 190  
 Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly  
 195 200 205  
 Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln  
 210 215 220  
 Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

FOR "SECRET"

[illegible]

Gly 515	Tyr	Ile	Leu	Arg	Glu	Asp	Gly 520	Lys	Thr	Cys	Arg	Arg 525	Lys	Asp	Val
Cys 530	Gln	Ala	Ile	Asp	His	Gly 535	Cys	Glu	His	Ile	Cys 540	Val	Asn	Ser	Asp
Asp 545	Ser	Tyr	Thr	Cys	Glu 550	Cys	Leu	Glu	Gly	Phe 555	Arg	Leu	Ala	Glu	Asp 560
Gly	Lys	Arg	Cys	Arg 565	Arg	Lys	Asp	Val	Cys 570	Lys	Ser	Thr	His	His 575	Gly
Cys	Glu	His	Ile 580	Cys	Val	Asn	Asn	Gly 585	Asn	Ser	Tyr	Ile	Cys 590	Lys	Cys
Ser	Glu	Gly 595	Phe	Val	Leu	Ala	Glu 600	Asp	Gly	Arg	Arg	Cys 605	Lys	Lys	Cys
Thr	Glu	Gly 610	Pro	Ile	Asp	Leu 615	Val	Phe	Val	Ile	Asp 620	Gly	Ser	Lys	Ser
Leu 625	Gly	Glu	Glu	Asn	Phe 630	Glu	Val	Val	Lys	Gln 635	Phe	Val	Thr	Gly	Ile 640
Ile	Asp	Ser	Leu	Thr 645	Ile	Ser	Pro	Lys	Ala 650	Ala	Arg	Val	Gly	Leu 655	Leu
Gln	Tyr	Ser	Thr 660	Gln	Val	His	Thr	Glu 665	Phe	Thr	Leu	Arg	Asn 670	Phe	Asn
Ser	Ala	Lys 675	Asp	Met	Lys	Lys	Ala 680	Val	Ala	His	Met	Lys 685	Tyr	Met	Gly
Lys 690	Gly	Ser	Met	Thr	Gly	Leu 695	Ala	Leu	Lys	His	Met 700	Phe	Glu	Arg	Ser
Phe 705	Thr	Gln	Gly	Glu	Gly 710	Ala	Arg	Pro	Leu	Ser 715	Thr	Arg	Val	Pro	Arg 720
Ala	Ala	Ile	Val	Phe 725	Thr	Asp	Gly	Arg	Ala 730	Gln	Asp	Asp	Val	Ser	Glu 735
Trp	Ala	Ser	Lys 740	Ala	Lys	Ala	Asn	Gly 745	Ile	Thr	Met	Tyr	Ala 750	Val	Gly
Val	Gly	Lys 755	Ala	Ile	Glu	Glu	Glu 760	Leu	Gln	Glu	Ile	Ala 765	Ser	Glu	Pro
Thr	Asn 770	Lys	His	Leu	Phe	Tyr 775	Ala	Glu	Asp	Phe	Ser 780	Thr	Met	Asp	Glu
Ile 785	Ser	Glu	Lys	Leu	Lys 790	Lys	Gly	Ile	Cys	Glu 795	Ala	Leu	Glu	Asp	Ser 800

Arg Tyr Arg  
915

23

22

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag

<210> 38

<212> DNA

<213> Home

ggagcgcgcc	tgggtgtcag	cggetcgget	ccgcgcacg	ctccggcgt	cgcgcagcct	60
cggcacctgc	aggtccgtgc	gtcccgcggc	tggcgccct	gactccgtcc	cggccaggga	120
gggccaatgat	ttccctcccg	gggcccctgg	tgaccaactt	gctgcggttt	ttgttccctgg	180
ggctgagtgc	cctcgcgccc	ccctcgcggg	cccagctgca	actgcacttg	cccgccaacc	240
ggttgcaggc	ggtggaggga	ggggaagtgg	tgttccagc	gtggtacacc	ttgcacgggg	300
aggtgtcttc	atcccagcca	tgggaggtgc	cctttgtgat	gtggttcttc	aaacagaaag	360
aaaaggagga	tcaggtgttg	tcctacatca	atggggtcac	aacaagcaaa	cctggagtat	420
ccttgggtcta	ctccatgccc	tcccggaaac	tgteccctgcg	gctggagggt	ctccaggaga	480
aagactctgg	cccctacagc	tgtccgtga	atgtgcaaga	caaacaaggc	aaatctaggg	540
gccacagcat	caaaacctta	gaactcaatg	tactggttcc	tccagctcct	ccatcctgcc	600
gtctccaggg	tgtgccccat	gtgggggcaa	acgtgacctc	gagctgccag	tctccaagga	660
gtaagcccg	tgtccaatac	cagtgggatc	ggcagcttcc	atccttccag	actttctttg	720
caccagcatt	agatgtcatc	cgtgggtctt	taagcctcac	caacctttcg	tcttccattg	780
ctggagtcta	tgtctgcaag	gcccacaatg	aggtgggcac	tgcccaatgt	aatgtgacgc	840
tggaagtgag	cacagggcct	ggagctgcag	tggttgctgg	agctgtttgt	ggtagccctgg	900
ttggactggg	gttgtctggc	gggctggctc	tcttgtagca	ccgcgggggc	aaggccctgg	960
aggagccagc	caatgatatc	aaggaggatg	ccattgctcc	cgggaccttg	ccctggccca	1020
agagctcaga	cacaatctcc	aagaatggga	ccctttctct	tgtcacctcc	gcacgagccc	1080
tccggccacc	ccatggccct	cccaggcctg	gtgcattgac	ccccacgccc	agtctctcca	1140
gccaggccct	gccctcacca	agactgccc	cgacagatgg	ggcccaccct	caaccaatat	1200
cccccatccc	tgggtggggt	tcttctcttg	gcttgagccg	catgggtgct	gtgcctgtga	1260
tgggtgcctgc	ccagagtoaa	gctggctctc	tggtagatg	acccaccac	tcattggcta	1320
aaggatttg	ggtctctcct	tcctataagg	gtcacctcta	gcacagaggc	ctgagtcag	1380
ggaaagagtc	acactcctga	cccttagtac	tctgccccca	cctctcttta	ctgtgggaaa	1440
accatctcag	taagacctaa	gtgtccagga	gacagaagga	gaagagggaag	tggatctgga	1500
attgggagga	gcctccaccc	acccctgact	cctccttatg	aagccagctg	ctgaaattag	1560
ctactcacca	agagtgagg	gcagagactt	ccagtcactg	agtctcccag	gcccccttga	1620
tctgtacccc	acccctatct	aacaccaccc	ttggctccca	ctccagctcc	ctgtattgat	1680
ataacctgtc	aggttggttt	gggttaggtt	tactggggca	gaggataggg	aatctcttat	1740
taaaactaac	atgaaatatg	tgttggtttc	atttgcaaat	ttaaataaag	atacataatg	1800
tttqtatgaa	aaa					1813

<211> 390

<212> PRT

<213> Home

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1	5	10	15
Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln	20	25	30
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val	35	40	45
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln	50	55	60
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys	65	70	75
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro	85	90	95
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg	100	105	110
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val	115	120	125
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr	130	135	140
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu	145	150	155
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser	165	170	175
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro	180	185	190
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser	195	200	205
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys	210	215	220
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu	225	230	235
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly	245	250	255
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His	260	265	270
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp	275	280	285

104420"99640660

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
 290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
 305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly  
 340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
 355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
 370 375 380

Gln Ala Gly Ser Leu Val  
 385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 40

aggggtctcca ggagaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 41

attgtggggcc ttgcagacat agac

24

<210> 42

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 42	
ggccacagca tcaaacctt agaactcaat gtactgggtc ctccagctcc	50
<210> 43	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 43	
gtgtgacaca gcgtgggc	18
<210> 44	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 44	
gaccggcagg cttctgcg	18
<210> 45	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 45	
cagcagcttc agccaccagg agtgg	25
<210> 46	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 46	
ctgagccgtg ggctgcagtc tcgc	24
<210> 47	



<211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 47

ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc

45

<210> 48

<211> 2822

<212> DNA

<213> Homo sapiens

<400> 48

```

cgccaccact gcggccaccg ccaatgaaac gcctcccgt cctagtgggt tttccactt 60
tggtgaattg ttccataact caaaattgca ccaagacacc ttgtctccca aatgcaaaat 120
gtgaaatacg caatggaatt gaagcctgct attgcaacat gggattttca ggaaatgggtg 180
tcacaatttg tgaagatgat aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240
ctaattgcac taacacagaa ggaagttatt attgtatgtg tgtacctggc ttcagatcca 300
gcagtaacca agacagggtt atcactaatg atggaaccgt ctgtatagaa aatgtgaatg 360
caaactgcc tttagataat gtctgtatag ctgcaaatat taataaaact ttaacaaaaa 420
tcagatccat aaaagaacct gtggctttgc tacaagaagt ctatagaaat tctgtgacag 480
atctttcacc aacagatata attacatata tagaaatatt agctgaatca tcttcattac 540
taggttacaa gaacaacact atctcagcca aggacacct ttctaactca actcttactg 600
aatttgtaaa aaccgtgaat aattttgttc aaagggatac atttgtagtt tgggacaagt 660
tatctgtgaa tcataggaga acacatctta caaaactcat gcacactggt gaacaagcta 720
ctttaaggat atcccagagc ttccaaaaga ccacagagtt tgatacaaat tcaacggata 780
tagctctcaa agttttcttt tttgattcat ataacatgaa acatattcat cctcatatga 840
atatggatgg agactacata aatatatttc caaagagaaa agctgcatat gattcaaatg 900
gcaatgttgc agttgcattt ttatattata agagtattgg tcctttgctt tcatcatctg 960
acaacttctt attgaaacct caaaattatg ataattctga agaggaggaa agagtcatat 1020
cttcagtaat ttcagttctc atgagctcaa acccaccac attatatgaa cttgaaaaaa 1080
taacatttac attaagtcac cgaaagggtc cagataggta taggagtcta tgtgcatttt 1140
ggaattactc acctgatacc atgaatggca gctgggtctt agagggctgt gagctgacat 1200
actcaaatga gaccacacc tcatgccgt gtaatcacct gacacatttt gcaattttga 1260
tgtcctctgg tccttccatt ggtattaaag attataatat tcttacaagg atcactcaac 1320
taggaataat tatttcaactg atttgtcttg ccatatgcat ttttaccttc tgggtcttca 1380
gtgaaattca aagcaccagg acaacaattc acaaaaatct ttgctgtagc ctatttcttg 1440
ctgaacttgt ttttcttggt gggatcaata caaatactaa taagctcttc tgttcaatca 1500
ttgccggact gctacactac ttcttttttag ctgcttttgc atggatgtgc attgaaggca 1560
tacatctcta tctcattggt gtgggtgtca tctacaacaa gggatttttg cacaagaatt 1620
tttatatctt tggtatctta agcccagccg tggtagttgg attttcggca gcactaggat 1680
acagatatta tggcacaacc aaagtatggt ggcttagcac cgaaaacaac tttatttgga 1740
gttttatagg accagcatgc ctaatcattc ttgttaatct cttggctttt ggagtcacat 1800
tatacaaagt ttttcgtcac actgcagggt tgaaaccaga agttagttgc tttgagaaca 1860
taaggtcttg tgcaagagga gccctcgctc ttctgttctt tctcgccacc acctggatct 1920
ttggggttct ccatgttgtg cagcatcag ttggttacagc ttacctcttc acagtcagca 1980
atgctttcca ggggatgttc atttttttat tctgtgtgtg tttatctaga aagattcaag 2040
aagaatatta cagattgttc aaaaatgtcc cctgttgttt tggatgttta aggtaaacat 2100
agagaatggt ggataattac aactgcacaa aaataaaaaat tccaagctgt ggatgaccaa 2160

```

```
<210> 49
<211> 690
<212> PRT
<213> Homo sapiens
```

```

<400> 49
Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys
  1                      5                      10                      15
Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
                20                      25                      30
Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
        35                      40                      45
Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
    50                      55                      60
Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
  65                      70                      75                      80
Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
                85                      90                      95
Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
        100                      105                      110
Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
        115                      120                      125
Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
    130                      135                      140
Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
  145                      150                      155                      160
Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
        165                      170                      175
Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

```

180 185 190  
 Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val  
 195 200 205  
 Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys  
 210 215 220  
 Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe  
 225 230 235 240  
 Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys  
 245 250 255  
 Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met  
 260 265 270  
 Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala  
 275 280 285  
 Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser  
 290 295 300  
 Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln  
 305 310 315 320  
 Asn Tyr Asp Asn Ser Glu Glu Glu Glu Arg Val Ile Ser Ser Val Ile  
 325 330 335  
 Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys  
 340 345 350  
 Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser  
 355 360 365  
 Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp  
 370 375 380  
 Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser  
 385 390 395 400  
 Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly  
 405 410 415  
 Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln  
 420 425 430  
 Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr  
 435 440 445  
 Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys  
 450 455 460

180 185 190  
 200 205  
 210 215 220  
 225 230 235 240  
 245 250 255  
 260 265 270  
 275 280 285  
 290 295 300  
 305 310 315 320  
 325 330 335  
 340 345 350  
 355 360 365  
 370 375 380  
 385 390 395 400  
 405 410 415  
 420 425 430  
 435 440 445  
 450 455 460

```
<210> 50
<211> 589
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (61)
```

<223> a, t, c or g

<400> 50

```

tggaacata tctccctca tatgaatatg gatggagact acataaatat atttccaaag 60
ngaaaagccg gcatatggat tcaaattggca atgttgcagt tgcattttta tattataaga 120
gtattggtec ctttgctttc atcatctgac aacttcttat tgaaacctca aaattatgat 180
aattctgaag aggaggaaa agtcatatct tcagtaattt cagtctcaat gagctcaaac 240
ccaccacat tatatgaact tgaaaaaata acatttacat taagtcacgc aaaggtcaca 300
gataggtata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360
tggtcttcag agggctgtga gctgacatac tcaaattgaga cccacacctc atgccgctgt 420
aatcacctga cacattttgc aattttgatg tctctgggtc cttccattgg tattaaagat 480
tataatattc ttacaaggat cactcaacta ggaataatta ttctactgat ttgtcttgcc 540
atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589

```

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 51

ggtaatgagc tccattacag 20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 52

ggagtagaaa gcgcatgg 18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag 22

<210> 54

<211> 18

<212> DNA

TOPIC "95040660"

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 55

ggatctcctg agctcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 56

cctagttgag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 57

atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

gctcccagcc aagaacctcg gggccgctgc gcggtgggga ggagttcccc gaaacccggc 60  
cgctaagcga ggctcctcc tcccgcagat ccgaacggcc tgggcggggc caccgccgct 120

Top 20 "SS640000"

gggacaagaa gccgcgcgct gcctgcccgg gcccggggag ggggctgggg ctggggccgg 180  
 aggcgggggtg tgagtgggtg tgtgcggggg ggggaggctt gatgcaatcc cgataagaaa 240  
 tgctcgggtg tcttgggcac ctaccgtgg ggcgcgtaag gcgctactat ataaggctgc 300  
 cggcccgag cgcgcgcgcc gtcagagcag gagcgctgcg tccaggatct agggccacga 360  
 ccatcccaac cgggcaactca cagccccgca ggcgatcccg gtgcgcgccc agcctcccgc 420  
 acccccatcg cgggagctgc gccgagagcc ccaggagggt gccatgcgga gcgggtgtgt 480  
 ggtggtccac gtatggatcc tggcgggct ctggtggcc gtggccgggc gccccctgc 540  
 cttctcggac gcggggcccc acgtgcaacta cggctggggc gaccccatcc gcctgcggca 600  
 cctgtacacc tccggccccc acgggtctctc cagctgcttc ctgcgcaccc gtgccgacgg 660  
 cgtcgtggac tgcgcgcggg gccagagcgc gcacagtctg ctggagatca aggcagtcgc 720  
 tctgcggacc gtggccatca agggcgtgca cagcgtgcgg tacctctgca tgggcgcga 780  
 cggcaagatg caggggctgc ttcagtactc ggagggaagac tgtgctttcg aggaggagat 840  
 ccgcccagat ggctacaatg tgtaccgatc cgagaagcac cgcctcccgg tctccctgag 900  
 cagtgccaaa cagcggcagc tgtacaagaa cagaggcttt cttccactct ctcatttct 960  
 gcccatgctg cccatggctc cagaggagcc tgaggacctc aggggccact tggaatctga 1020  
 catgttctct tcgcccctgg agaccgacag catggacca tttgggcttg tcaccggact 1080  
 ggaggccgtg aggagtccca gctttgagaa gtaactgaga ccatgcccgg gcctcttcac 1140  
 tgctgccagg ggctgtggtg cctgcagcgt gggggacgtg cttctacaag aacagtcttg 1200  
 agtccacggt ctgtttagct ttaggaagaa acatctagaa gttgtacata ttcagagttt 1260  
 tccattggca gtgccagttt ctagccaata gacttgtctg atcataacat tgtaaacctg 1320  
 tagcttgccc agctgctgcc tgggccccca ttctgctccc tcgaggttgc tggacaagct 1380  
 gctgcactgt ctcagttctg cttgaatacc tccatcgatg gggaaactcac ttcctttgga 1440  
 aaaattctta tgtcaagctg aaattctcta atttttctc atcaactccc caggagcagc 1500  
 cagaagacag gcagtagttt taatttcagg aacagggtgat ccactctgta aaacagcagg 1560  
 taaatttcac tcaaccccat gtgggaattg atctatatct ctacttccag ggaccatttg 1620  
 ccttcccaa atccctccag gccagaactg actggagcag gcatggccca ccaggcttca 1680  
 ggagtagggg aagcctggag cccactcca gccctgggac aacttgagaa tccccctga 1740  
 ggccagttct gtcattggat ctgtcctgag aataacttgc tgtcccgggtg tcacctgctt 1800  
 ccatctccca gccaccagc cctctgccc cctcacatgc ctccccatgg attggggcct 1860  
 cccaggcccc ccaccttatg tcaacctgca cttcttggtc aaaaatcagg aaaagaaaag 1920  
 atttgaagac cccaagtctt gtcaataact tgcgtgtgtg aagcagcggg ggaagacct 1980  
 gaacccttcc cccagcactt ggttttccaa catgatatt atgagtaatt tattttgata 2040  
 tgtacatctc ttattttctt acattattta tgccccaaa ttatatttat gtatgtaagt 2100  
 gaggtttgtt ttgtatatta aaatggagtt tgtttgt 2137

<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu  
 1 5 10 15

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro  
 20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr  
 35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala  
 50 55 60

FOR "99640000"

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
65 70 75 80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
85 90 95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
100 105 110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
115 120 125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
130 135 140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
145 150 155 160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
195 200 205

Val Arg Ser Pro Ser Phe Glu Lys  
210 215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 60

atccgcccag atggctacaa tgtgta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 61

gcctcccggc ctccctgagc agtgccaaac agcggcagtg ta

42



<210> 62  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 62  
 ccagtcgggt gacaagccca aa

22

<210> 63  
 <211> 1295  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
 cccagaagtt caagggcccc cggcctcctg cgctcctgcc gccgggaccc tcgacctcct 60  
 cagagcagcc ggctgcccgc ccgggaagat ggcgaggagg agccgccacc gcctcctcct 120  
 gctgctgctg cgctacctgg tggtcgccct gggctatcat aaggcctatg ggttttctgc 180  
 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggctatgt tagcctgcaa 240  
 aaccccaag aagactgttt cctccagatt agagtggagg aaactgggtc ggagtgtctc 300  
 ctttgtctac tatcaacaga ctcttcaagg tgattttaaa aatcgagctg agatgataga 360  
 tttcaatatc cggatcaaaa atgtgacaag aagtgatgag gggaaatatc gttgtgaagt 420  
 tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tgggaagtatt 480  
 agtggctcca gcagttccat catgtgaagt accctcttct gctctgagtg gaactgtggt 540  
 agagctacga tgtcaagaca aagaaggga tccagctcct gaatacacat ggtttaagga 600  
 tggcatccgt ttgctagaaa atcccagact tggctcccaa agcaccaaca gctcatacac 660  
 aatgaatata aaaactggaa ctctgcaatt taatactgtt tccaaactgg aactggaga 720  
 atattcctgt gaagcccga attctgttgg atatcgagg tgcctggga aacgaatgca 780  
 agtagatgat ctcaacataa gtggcatcat agcagccgta gtagttgtgg ccttagtgat 840  
 ttccgtttgt ggccttggtg tatgctatgc tcagaggaaa ggctactttt caaaagaaac 900  
 ctccctccag aagagtaatt ctcatctaa agccacgaca atgagtgaat atgtgcagtg 960  
 gctcacgcct gtaatcccag cactttggaa ggccgcggcg ggccggtcac gaggtcagga 1020  
 gttctagacc agtctggcca atatggtgaa accccatctc tactaaaata caaaaattag 1080  
 ctgggcatgg tggcatgtgc ctgcagttcc agctgcttgg gagacaggag aatcacttga 1140  
 acccgggagg cggagggttc agtgagctga gatcacgcca ctgcagtcca gcctgggtaa 1200  
 cagagcaaga ttccatctca aaaaataaaa taaataaata aataaatact ggtttttacc 1260  
 tgtagaattc ttacaataaa tatagcttga tattc 1295

<210> 64  
 <211> 312  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
 Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr  
 1 5 10 15  
 Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro  
 20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu  
 35 40 45  
 Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys  
 50 55 60  
 Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
 65 70 75 80  
 Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
 85 90 95  
 Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
 100 105 110  
 Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
 115 120 125  
 Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
 130 135 140  
 Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
 145 150 155 160  
 Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
 165 170 175  
 Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
 180 185 190  
 Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp  
 195 200 205  
 Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg  
 210 215 220  
 Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile  
 225 230 235 240  
 Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu  
 245 250 255  
 Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser  
 260 265 270  
 Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn  
 275 280 285  
 Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala  
 290 295 300  
 Gly Gly Ser Arg Gly Gln Glu Phe

T  
O  
T  
A  
L  
S  
E  
Q  
U  
E  
N  
C  
E

310

<211> 22

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 65

atcgttgtga agttagtgcc cc

22

<210> 66

<211> 23

<212> DNA

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 66

acctgcgata tccaacagaa ttg

23

<210> 67

<211> 48

<212> DNA

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 67

ggaagaggat acagtcactc tggaagtatt agtggctcca gcaqttcc

48

<210> 68

<211> 2639

<212> DNA

<213> Homo sapiens

<400> 68

gacatcggag	gtgggctagc	actgaaactg	cttttcaaga	cgaggaagag	gaggagaaag	60
agaaagaaga	ggaagatggt	gggcaacatt	tattttaacat	gctccacagc	cgggacctg	120
gcatcatgct	gctatttctg	caaatactga	agaagcatgg	gattttaaata	ttttactttct	180
aaataaatga	attactcaat	ctcctatgac	catctataca	tactccacct	tcaaaaagta	240
catcaatatt	atatcattaa	ggaaatagta	accttctctt	ctccaatatg	catgacattt	300
ttggacaatg	caattgtggc	actggcactt	atttcagtga	agaaaaactt	tgtggttcta	360
tggcattcat	catttgacaa	atgcaagcat	cttccttatc	aatcagctcc	tattgaaact	420
actagcactg	actgtggaat	ccttaagggc	ccattacatt	tctgaagaag	aaagctaaga	480
tgaaggacat	gccactccga	attcatgtgc	tacttggcct	agctatcact	acactagtac	540

```
<210> 69
<211> 708
<212> PRT
<213> Homo sapiens
```

<400> 69  
Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile  
1 5 10 15  
Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu  
20 25 30  
Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met  
35 40 45  
Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro  
50 55 60

[illegible]

			340				345				350				
Thr	Ile	Glu	Ser	Leu	Pro	Asn	Leu	Lys	Glu	Ile	Ser	Ile	His	Ser	Asn
		355				360						365			
Pro	Ile	Arg	Cys	Asp	Cys	Val	Ile	Arg	Trp	Met	Asn	Met	Asn	Lys	Thr
		370				375						380			
Asn	Ile	Arg	Phe	Met	Glu	Pro	Asp	Ser	Leu	Phe	Cys	Val	Asp	Pro	Pro
385				390						395				400	
Glu	Phe	Gln	Gly	Gln	Asn	Val	Arg	Gln	Val	His	Phe	Arg	Asp	Met	Met
				405				410						415	
Glu	Ile	Cys	Leu	Pro	Leu	Ile	Ala	Pro	Glu	Ser	Phe	Pro	Ser	Asn	Leu
		420				425						430			
Asn	Val	Glu	Ala	Gly	Ser	Tyr	Val	Ser	Phe	His	Cys	Arg	Ala	Thr	Ala
		435				440						445			
Glu	Pro	Gln	Pro	Glu	Ile	Tyr	Trp	Ile	Thr	Pro	Ser	Gly	Gln	Lys	Leu
450						455						460			
Leu	Pro	Asn	Thr	Leu	Thr	Asp	Lys	Phe	Tyr	Val	His	Ser	Glu	Gly	Thr
465				470						475				480	
Leu	Asp	Ile	Asn	Gly	Val	Thr	Pro	Lys	Glu	Gly	Gly	Leu	Tyr	Thr	Cys
				485				490						495	
Ile	Ala	Thr	Asn	Leu	Val	Gly	Ala	Asp	Leu	Lys	Ser	Val	Met	Ile	Lys
		500						505				510			
Val	Asp	Gly	Ser	Phe	Pro	Gln	Asp	Asn	Asn	Gly	Ser	Leu	Asn	Ile	Lys
		515				520						525			
Ile	Arg	Asp	Ile	Gln	Ala	Asn	Ser	Val	Leu	Val	Ser	Trp	Lys	Ala	Ser
530						535						540			
Ser	Lys	Ile	Leu	Lys	Ser	Ser	Val	Lys	Trp	Thr	Ala	Phe	Val	Lys	Thr
545				550						555				560	
Glu	Asn	Ser	His	Ala	Ala	Gln	Ser	Ala	Arg	Ile	Pro	Ser	Asp	Val	Lys
				565				570						575	
Val	Tyr	Asn	Leu	Thr	His	Leu	Asn	Pro	Ser	Thr	Glu	Tyr	Lys	Ile	Cys
		580				585						590			
Ile	Asp	Ile	Pro	Thr	Ile	Tyr	Gln	Lys	Asn	Arg	Lys	Lys	Cys	Val	Asn
		595				600						605			
Val	Thr	Thr	Lys	Gly	Leu	His	Pro	Asp	Gln	Lys	Glu	Tyr	Glu	Lys	Asn
610				615						620					

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile  
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
690 695 700

Thr Asn Met Ser  
705

<210> 70

<211> 1305

<212> DNA

<213> Homo sapiens

<400> 70

```

gcccgggact ggcgcaaggt gcccaagcaa ggaaagaaat aatgaagaga cacatgtgtt 60
agctgcagcc ttttgaaaca cgcaagaagg aaatcaatag tgtggacagg gctggaacct 120
ttaccacgct tgttggagta gatgaggaat gggctcgtga ttatgctgac attccagcat 180
gaatctggta gacctgtggt taaccctgttc cctctccatg tgtctcctcc tacaaagttt 240
tgttcttatg atactgtgct ttcattctgc cagtatgtgt cccaagggct gtctttgttc 300
tctctctggg ggtttaaatg tcacctgtag caatgcaaat ctcaaggaaa tacctagaga 360
tcttctctct gaaacagtct tactgtatct ggactccaat cagatcacat ctattcccaa 420
tgaaattttt aaggacctcc atcaactgag agttctcaac ctgtccaaaa atggcattga 480
gtttatcgat gagcatgcct tcaaaggagt agctgaaacc ttgcagactc tggacttgtc 540
cgacaatcgg attcaaagtg tgcacaaaaa tgccttcaat aacctgaagg ccagggccag 600
aattgccaac aacctctggc actgcgactg tactctacag caagtctctga ggagcatggc 660
gtccaatcat gagacagccc acaactgat ctgtaaaacg tccgtgttg atgaacatgc 720
tggcagacca ttctcaatg ctgccaacga cgctgacctt tgtaacctcc ctaaaaaaac 780
taccgattat gccatgctgg tcacctggtt tggctggttc actatggtga tctcatatgt 840
ggtatattat gtgaggcaaa atcaggagga tgcccggaga cacctcgaat acttgaaatc 900
cctgccaaagc aggcagaaga aagcagatga acctgatgat attagcactg tggatatagt 960
tccaaactga ctgtcattga gaaagaaaga aagtagtttg cgattgcagt agaaataagt 1020
ggtttacttc tccatccat tgtaaacatt tgaaactttg tatttcagtt ttttttgaat 1080
tatgccactg ctgaactttt acaaacact acaacataaa taatttgagt ttaggtgatc 1140
cacccttaa ttgtaccccc gatggtatat ttctgagtaa gctactatct gaacattagt 1200
tagatccatc tcaatattta ataataaaat ttatTTTTTT aatttaaaaag caaataaaaag 1260
cttaactttg aaccatggga aaaaaaaaaa aaaaaaaaaa aaaca 1305

```

<210> 71

<211> 259

<212> PRT

<213> Homo sapiens

<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu  
 1 5 10 15  
 Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser  
 20 25 30  
 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val  
 35 40 45  
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60  
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
 65 70 75 80  
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95  
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110  
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125  
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
 130 135 140  
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
 145 150 155 160  
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
 165 170 175  
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
 180 185 190  
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
 195 200 205  
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
 210 215 220  
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
 225 230 235 240  
 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser  
 245 250 255  
 Thr Val Val

&lt;210&gt; 72

&lt;211&gt; 2290

T07120 95640660



<212> DNA  
 <213> Homo sapiens

<400> 72

```

accgagccga ggggaccgaa ggcgcgccc agatgcaggt gagcaagagg atgctggcgg 60
ggggcgtgag gagcatgccc agccccctcc tggcctgctg gcagcccatc ctccctgctgg 120
tgctgggctc agtgcctgca ggctcggcca cgggctgccc gcccgcctgc gaggctccg 180
cccaggaccg cgtcgtgctg tgccaccgca agtgccttgc ggcagtcctc gagggcaccc 240
ccaccgagac gcgcctgctg gacctaggca agaaccgcat caaaacgctc aaccaggacg 300
agttcgccag ctcccgccac ctggaggagc tggagctcaa cgagaacatc gtgagcgccg 360
tggagcccg ggccttcaac aacctcttca acctccggac gctgggtctc cgcagcaacc 420
gcctgaagct catcccgcta ggctcttca ctggcctcag caacctgacc aagcaggaca 480
tcagcgagaa caagatcggt atcctactgg actacatggt tcaggacctg tacaacctca 540
agtcactgga ggttgccgac aatgacctcg tctacatctc tcaccgcgcc ttcagcgggc 600
tcaacagcct ggagcagctg acgctggaga aatgcaacct gacctccatc cccaccgagg 660
cgctgtccca cctgcacggc ctcatcgccc tgaggtcccg gcacctcaac atcaatgcca 720
tccgggacta ctccctcaag aggtcgtacc gactcaaggt cttggagatc tccactggc 780
cctacttgga caccatgaca cccaactgcc tctacggcct caacctgacg tccctgtcca 840
tcacacactg caatctgacc gctgtgccct acctggccgt ccgccacctc gtctatctcc 900
gcttccctca cctctctac aacccccatc gcaccattga gggctccatg ttgcatgagc 960
tgctccggct gcaggagatc cagctgggtg gggggcagct gggcgtgggt gagccctatg 1020
ccttcgcggg cctcaactac ctgcgcgtgc tcaatgtctc tggcaaccag ctgaccacac 1080
tggaggaatc agtcttccac tccgtgggca acctggagac actcatcctg gactccaacc 1140
cgctggcctg cgaactgtcg ctccctgtgg tgttcggcg ccgctggcg ctcaacttca 1200
accggcagca gcccacgtgc gccacgccc agtttgtcca gggcaaggag ttcaaggact 1260
tccctgatgt gctactgccc aactacttca cctgcgcgcg cggccgcac cgggaccgca 1320
aggcccagca ggtgtttgtg gacgagggcc acacggtgca gtttgtgtgc cgggcccgatg 1380
gcgaccgcgc gcccgcctc ctctggctct caccgccaaa gcacctgggt tcagccaaga 1440
gcaatgggcg gctcacagtc ttccctgatg gcacgctgga ggtgcgctac gccagggtac 1500
aggacaacgg cacgtacctg tgcctgcggg ccaacgcggg cggcaaccgac tccatgcccg 1560
cccacctgca tgtgcgcagc tactcgccc actggcccca tcagcccaac aagaccttcg 1620
ctttcatctc caaccagccg ggcgagggag agggcaacag caccgcgcgc actgtgcctt 1680
tcccttccga catcaagacc ctcatcatcg ccaccaccat gggcttcac tcttctctgg 1740
gcgtcgtcct cttctgcctg gtgctgctgt ttctctggag ccggggcaag ggcaacacaa 1800
agcacaacat cgagatcgag tatgtgcccc gaaagtcgga cgcaggcatc agctccgccc 1860
acgcgccccg caagttcaac atgaagatga tatgagggcg gggcgggggg cagggacccc 1920
cgggcggccg ggcaggggaa ggggcctggt cgcacctgc tcaactctca gtcttccca 1980
cctcctccct acccttctac aacggttctc tttctccctc ccgcctccgt cccctgctgc 2040
ccccgcag cctcaccac ctgcctcct tctaccagga cctcagaagc ccagacctgg 2100
ggacccacc tacacagggg cattgacaga ctggagttga aagccgacga accgacacgc 2160
ggcagagtca ataattcaat aaaaaagtta cgaactttct ctgtaacttg ggtttcaata 2220
attatggatt tttatgaaaa cttgaaataa taaaaagaga aaaaaactaa aaaaaaaaaa 2280
aaaaaaaaa 2290

```

<210> 73  
 <211> 620  
 <212> PRT  
 <213> Homo sapiens

<400> 73

```

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro
  1                      5                      10                      15

```

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly  
 20 25 30  
 Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys  
 35 40 45  
 Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala  
 50 55 60  
 Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys  
 65 70 75 80  
 Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His  
 85 90 95  
 Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro  
 100 105 110  
 Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser  
 115 120 125  
 Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn  
 130 135 140  
 Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp  
 145 150 155 160  
 Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp  
 165 170 175  
 Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser  
 180 185 190  
 Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr  
 195 200 205  
 Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His  
 210 215 220  
 Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg  
 225 230 235 240  
 Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr  
 245 250 255  
 Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His  
 260 265 270  
 Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr  
 275 280 285  
 Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly  
 290 295 300

FOI b7 - 990660

Ser	Met	Leu	His	Glu	Leu	Leu	Arg	Leu	Gln	Glu	Ile	Gln	Leu	Val	Gly
305					310					315					320
Gly	Gln	Leu	Ala	Val	Val	Glu	Pro	Tyr	Ala	Phe	Arg	Gly	Leu	Asn	Tyr
				325					330					335	
Leu	Arg	Val	Leu	Asn	Val	Ser	Gly	Asn	Gln	Leu	Thr	Thr	Leu	Glu	Glu
			340					345					350		
Ser	Val	Phe	His	Ser	Val	Gly	Asn	Leu	Glu	Thr	Leu	Ile	Leu	Asp	Ser
		355					360					365			
Asn	Pro	Leu	Ala	Cys	Asp	Cys	Arg	Leu	Leu	Trp	Val	Phe	Arg	Arg	Arg
	370					375					380				
Trp	Arg	Leu	Asn	Phe	Asn	Arg	Gln	Gln	Pro	Thr	Cys	Ala	Thr	Pro	Glu
385					390					395					400
Phe	Val	Gln	Gly	Lys	Glu	Phe	Lys	Asp	Phe	Pro	Asp	Val	Leu	Leu	Pro
				405					410					415	
Asn	Tyr	Phe	Thr	Cys	Arg	Arg	Ala	Arg	Ile	Arg	Asp	Arg	Lys	Ala	Gln
			420					425					430		
Gln	Val	Phe	Val	Asp	Glu	Gly	His	Thr	Val	Gln	Phe	Val	Cys	Arg	Ala
		435					440					445			
Asp	Gly	Asp	Pro	Pro	Pro	Ala	Ile	Leu	Trp	Leu	Ser	Pro	Arg	Lys	His
	450					455					460				
Leu	Val	Ser	Ala	Lys	Ser	Asn	Gly	Arg	Leu	Thr	Val	Phe	Pro	Asp	Gly
465					470					475					480
Thr	Leu	Glu	Val	Arg	Tyr	Ala	Gln	Val	Gln	Asp	Asn	Gly	Thr	Tyr	Leu
				485					490					495	
Cys	Ile	Ala	Ala	Asn	Ala	Gly	Gly	Asn	Asp	Ser	Met	Pro	Ala	His	Leu
			500					505					510		
His	Val	Arg	Ser	Tyr	Ser	Pro	Asp	Trp	Pro	His	Gln	Pro	Asn	Lys	Thr
		515					520					525			
Phe	Ala	Phe	Ile	Ser	Asn	Gln	Pro	Gly	Glu	Gly	Glu	Ala	Asn	Ser	Thr
		530				535					540				
Arg	Ala	Thr	Val	Pro	Phe	Pro	Phe	Asp	Ile	Lys	Thr	Leu	Ile	Ile	Ala
545					550					555					560
Thr	Thr	Met	Gly	Phe	Ile	Ser	Phe	Leu	Gly	Val	Val	Leu	Phe	Cys	Leu
				565					570					575	
Val	Leu	Leu	Phe	Leu	Trp	Ser	Arg	Gly	Lys	Gly	Asn	Thr	Lys	His	Asn

Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile  
610 615 620

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

```
<210> 75
<211> 23
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

```
<210> 76
<211> 52
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
```

[illegible]

```
<210> 77
<211> 22
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
```

[illegible]

<400> 77  
ccatgtgtct cctcctacaa ag 22

<210> 78  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 78  
gggaatagat gtgatctgat tgg 23

<210> 79  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 79  
cacctgtagc aatgcaaatc tcaaggaaat acctagagat cttcctcctg 50

<210> 80  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 80  
agcaaccgcc tgaagctcat cc 22

<210> 81  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 81  
aaggcgcggt gaaagatgta gacg 24

<210> 82

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 82  
 gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga 50

<210> 83  
 <211> 1685  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
 cccacgcgtc cgcacctcgg ccccggggtc cgaagcggct cggggggcgcc ctttcgggtca 60  
 acatcgtagt ccacccccctc cccatcccca gcccccgagg attcaggctc gccagcgccc 120  
 agccagggag ccggccggga agcgcgatgg gggccccagc cgcctcgtct ctgctcctgc 180  
 tcttgctgtt cgcctgctgc tgggcgcccc gcggggcca cctctcccag gacgacagcc 240  
 agccctggac atctgatgaa acagtgggtg ctggtggcac cgtggtgctc aagtgccaaag 300  
 tgaaagatca cgaggactca tccttgcaat ggtctaacct tgctcagcag actctctact 360  
 ttggggagaa gagagccctt cgagataatc gaattcagct gggtacctct acgccccacg 420  
 agctcagcat cagcatcagc aatgtggccc tggcagacga gggcgagtag acctgctcaa 480  
 tcttcactat gcctgtgcga actgccaaagt ccctcgtcac tgtgctagga attccacaga 540  
 agcccatcat cactgggttat aaatcttcat tacgggaaaa agacacagcc accctaaact 600  
 gtcagtcttc tgggagcaag cctgcagccc ggctcacctg gagaaagggt gaccaagaac 660  
 tccacggaga accaaccgac atacaggaag atcccaatgg taaaaccttc actgtcagca 720  
 gctcggtagc attccagggt acccgggagg atgatggggc gagcatcgtg tgctctgtga 780  
 accatgaatc tctaaaggga gctgacagat ccacctctca acgcattgaa gttttatata 840  
 caccaactgc gatgattagg ccagacctc cccatcctcg tgagggccag aagctgttgc 900  
 tacactgtga gggtcgcggc aatccagtc cccagcagta cctatgggag aaggagggca 960  
 gtgtgccacc cctgaagatg acccaggaga gtgcctgat ctccctttc ctcaacaaga 1020  
 gtgacagtgg cacctacggc tgcacagcca ccagcaacat gggcagctac aaggcctact 1080  
 acaccctcaa tgtaatgac cccagtcagg tgcctcctc ctccagcacc taccacgcca 1140  
 tcatcggtgg gatcggtgct ttcattgtct tctgctgct catcatgctc atcttctctg 1200  
 gccactactt gatccggcac aaaggaacct acctgacaca tgaggcaaaa ggctccgacg 1260  
 atgctccaga cgcggacacg gccatcatca atgcagaagg cgggcagtcg ggaggggacg 1320  
 acaagaagga atatttcate tagaggcgcc tgcccacttc ctgcgcccc cagggggcct 1380  
 gtggggactg ctggggcgt caccaaccg gacttgtaga gagcaaccgc agggccgccc 1440  
 ctcccgttg ctcccagcc caccacccc cctgtacaga atgtctgctt tgggtgctgt 1500  
 tttgtactcg gtttggaatg gggagggagg agggcgggg gaggggaggg ttgccctcag 1560  
 cctttccgt ggcttctctg catttgggtt attattatt ttgtaacaat cccaaatcaa 1620  
 atctgtctcc aggcaggaga ggcaggagcc ctggggtgag aaaagcaaaa aacaaacaaa 1680  
 aaaca 1685

<210> 84  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 84

Met	Gly	Ala	Pro	Ala	Ala	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Phe	Ala	1	5	10	15	
Cys	Cys	Trp	Ala	Pro	Gly	Gly	Ala	Asn	Leu	Ser	Gln	Asp	Asp	Ser	Gln	20	25	30	
Pro	Trp	Thr	Ser	Asp	Glu	Thr	Val	Val	Ala	Gly	Gly	Thr	Val	Val	Leu	35	40	45	
Lys	Cys	Gln	Val	Lys	Asp	His	Glu	Asp	Ser	Ser	Leu	Gln	Trp	Ser	Asn	50	55	60	
Pro	Ala	Gln	Gln	Thr	Leu	Tyr	Phe	Gly	Glu	Lys	Arg	Ala	Leu	Arg	Asp	65	70	75	80
Asn	Arg	Ile	Gln	Leu	Val	Thr	Ser	Thr	Pro	His	Glu	Leu	Ser	Ile	Ser	85	90	95	
Ile	Ser	Asn	Val	Ala	Leu	Ala	Asp	Glu	Gly	Glu	Tyr	Thr	Cys	Ser	Ile	100	105	110	
Phe	Thr	Met	Pro	Val	Arg	Thr	Ala	Lys	Ser	Leu	Val	Thr	Val	Leu	Gly	115	120	125	
Ile	Pro	Gln	Lys	Pro	Ile	Ile	Thr	Gly	Tyr	Lys	Ser	Ser	Leu	Arg	Glu	130	135	140	
Lys	Asp	Thr	Ala	Thr	Leu	Asn	Cys	Gln	Ser	Ser	Gly	Ser	Lys	Pro	Ala	145	150	155	160
Ala	Arg	Leu	Thr	Trp	Arg	Lys	Gly	Asp	Gln	Glu	Leu	His	Gly	Glu	Pro	165	170	175	
Thr	Arg	Ile	Gln	Glu	Asp	Pro	Asn	Gly	Lys	Thr	Phe	Thr	Val	Ser	Ser	180	185	190	
Ser	Val	Thr	Phe	Gln	Val	Thr	Arg	Glu	Asp	Asp	Gly	Ala	Ser	Ile	Val	195	200	205	
Cys	Ser	Val	Asn	His	Glu	Ser	Leu	Lys	Gly	Ala	Asp	Arg	Ser	Thr	Ser	210	215	220	
Gln	Arg	Ile	Glu	Val	Leu	Tyr	Thr	Pro	Thr	Ala	Met	Ile	Arg	Pro	Asp	225	230	235	240
Pro	Pro	His	Pro	Arg	Glu	Gly	Gln	Lys	Leu	Leu	Leu	His	Cys	Glu	Gly	245	250	255	
Arg	Gly	Asn	Pro	Val	Pro	Gln	Gln	Tyr	Leu	Trp	Glu	Lys	Glu	Gly	Ser	260	265	270	
Val	Pro	Pro	Leu	Lys	Met	Thr	Gln	Glu	Ser	Ala	Leu	Ile	Phe	Pro	Phe	275	280	285	

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
 305 310 315 320

Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Asn Ala Glu  
 370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
 385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 85

gctaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

004120-99640650



26

50

50

<400>	90						
ggggggttagg	gaggaaggaa	tccaccccca	ccccccaaa	ccctttttctt	ctccttttctt	60	
ggcttcggac	attggagcac	taaatagaact	tgaattgtgt	ctgtggcgag	caggatggtc	120	
gctgttactt	tgtgatgaga	tgggggatga	attgctcgct	ttaaaaatgc	tgctttggat	180	
tctgttgctg	gagacgtctc	tttgttttgc	cgctggaaac	gttacagggg	acgtttgcaa	240	
agagaagatc	tgttcctgca	atgagataga	aggggacctt	cacgtagact	gtgaaaaaaa	300	
gggcttcaca	agtctgcagc	gtttcactgc	cccgaacttc	cagtttttacc	atttattttct	360	
gcatggcaat	tccctcactc	gacttttccc	taatgagttc	gctaactttt	ataatgcggt	420	
tagtttgcac	atggaaaaca	atggcttgca	tgaaatcggt	ccggggggctt	ttctggggct	480	
gcagctggtg	aaaaggctgc	acatcaacaa	caacaagatc	aagtcttttc	gaaagcagac	540	
ttttctgggg	ctggacgcat	tggaaatatc	ccaggetgat	tttaattttat	tacgagatat	600	
agaccggggg	gccttcacag	acttgaacca	gctggaggtg	ctcatttttaa	atgacaatat	660	
catcagcacc	ctacctgcca	acgtgtttcca	gtatgtgccc	atcaccacc	tcgacctccg	720	
gggtaacagg	ctgaaaacgc	tgccttatga	ggaggtcttg	gagcaaattcc	ctggtaattgc	780	
ggagatcctg	ctagaggata	acccttggga	ctgcacctgt	gatctgctct	cctgtaaaaga	840	
atggctggaa	aacatttcca	agaatgcctt	gatcggccga	gtggctctgcy	aagccccccac	900	
cagactgcag	ggtaaagacc	tcaatgaaac	caccgaacag	gacttgtgtc	ctttgaaaaa	960	
ccgagtggat	tctagtctcc	cggcgcccc	tgcccaagaa	gagacctttg	ctcctggacc	1020	
cctgccaaact	cctttcaaga	caaatgggca	agaggatcat	gccacaccag	gggtctgctcc	1080	

aaacggaggt acaaagatcc caggcaactg gcagatcaaa atcagaccca cagcagcgat 1140  
 agcgacgggt agctccagga acaaaccctt agctaacagt ttaccctgcc ctgggggctg 1200  
 cagctgcgac cacatcccag ggtcggggtt aaagatgaac tgcaacaaca ggaacgtgag 1260  
 cagcttggct gatttgaagc ccaagctctc taacgtgcag gagcttttcc tacgagataa 1320  
 caagatccac agcatccgaa aatcgcactt tgtggattac aagaacctca ttctgttgga 1380  
 tctgggcaac aataacatcg ctactgtaga gaacaacact ttcaagaacc ttttggacct 1440  
 caggtggcta tacatggata gcaattacct ggacacgctg tcccgggaga aattcgcggg 1500  
 gctgcaaaac ctagagtacc tgaacgtgga gtacaacgct atccagctca tcctcccggg 1560  
 cactttcaat gccatgcccc aactgaggat cctcattctc aacaacaacc tgetgaggtc 1620  
 cctgctgtg gacgtgttcg ctgggggtctc gctctctaaa ctacgctgc acaacaatta 1680  
 cttcatgtac ctcccgttg caggggtgct ggaccagtta acctccatca tccagataga 1740  
 cctccacgga aaccctggg agtgcctctg cacaattgtg cttttcaagc agtgggcaga 1800  
 acgcttgggt tccgaagtgc tgatgagcga cctcaagtgt gagacgcggg tgaacttctt 1860  
 tagaaaggat ttcatgctcc tctccaatga cgagatctgc cctcagctgt acgctaggat 1920  
 ctgccccacg ttaacttcgc acagtaaaaa cagcactggg ttggcggaga cggggacgca 1980  
 ctccaactcc tacctagaca ccagcagggt gtccatctcg gtgttggtcc cgggactgct 2040  
 gctggtgttt gtcacctccg ccttcaccgt ggtgggcatg ctcggtgtta tcctgaggaa 2100  
 ccgaaagcgg tccaagagac gagatgccaa ctctcccgcg tccgagatta attccctaca 2160  
 gacagtctgt gactcttcct actggcaca tgggccttac aacgcagatg gggcccacag 2220  
 agtgtatgac tgtggctctc actcgctctc agactaagac cccaacccca ataggggagg 2280  
 gcagagggaa ggcgatacat cttcccccac cgcaggcacc ccgggggctg gaggggcgtg 2340  
 tacccaaadc cccgcgccat cagcctggat gggcataagt agataaataa ctgtgagctc 2400  
 gcacaaccga aagggcctga ccccttactt agctccctcc ttgaaacaaa gagcagactg 2460  
 tggagagctg ggagagcgca gccagctcgc tctttgctga gagccccttt tgacagaaa 2520  
 ccagcacga ccctgctgga agaactgaca gtgcctcgc cctcgcccc ggggcctgtg 2580  
 gggttggatg ccgcggttct atacatatat acatatatcc acatctatat agagagatag 2640  
 atatctattt tccccctgtg gattagcccc gtgatggctc cctgttggct acgcagggat 2700  
 gggcagttgc acgaaggcat gaatgtattg taaataagta actttgactt ctgac 2755

<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala  
 1 5 10 15

Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn  
 20 25 30

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr  
 35 40 45

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe  
 50 55 60

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn  
 65 70 75 80

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu  
 85 90 95

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His  
 100 105 110  
 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly  
 115 120 125  
 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp  
 130 135 140  
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile  
 145 150 155 160  
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr  
 165 170 175  
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu  
 180 185 190  
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu  
 195 200 205  
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys  
 210 215 220  
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val  
 225 230 235 240  
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr  
 245 250 255  
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro  
 260 265 270  
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr  
 275 280 285  
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala  
 290 295 300  
 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg  
 305 310 315 320  
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala  
 325 330 335  
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly  
 340 345 350  
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala  
 355 360 365  
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp  
 370 375 380

100  
 110  
 120  
 130  
 140  
 150  
 160  
 170  
 180  
 190  
 200  
 210  
 220  
 230  
 240  
 250  
 260  
 270  
 280  
 290  
 300  
 310  
 320  
 330  
 340  
 350  
 360  
 370  
 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
 385 390 395 400  
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn  
 405 410 415  
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser  
 420 425 430  
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn  
 435 440 445  
 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro  
 450 455 460  
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
 465 470 475 480  
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu  
 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
 500 505 510  
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
 515 520 525  
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala  
 530 535 540  
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
 545 550 555 560  
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
 565 570 575  
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
 580 585 590  
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
 595 600 605  
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
 610 615 620  
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
 625 630 635 640  
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
 645 650 655  
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

385 390 395 400  
 405 410 415  
 420 425 430  
 435 440 445  
 450 455 460  
 465 470 475 480  
 485 490 495  
 500 505 510  
 515 520 525  
 530 535 540  
 545 550 555 560  
 565 570 575  
 580 585 590  
 595 600 605  
 610 615 620  
 625 630 635 640  
 645 650 655

660 665 670  
 Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp  
 675 680 685  
 Cys Gly Ser His Ser Leu Ser Asp  
 690 695  
 <210> 92  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
 <400> 92  
 gttggatctg ggcaacaata ac 22  
 <210> 93  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
 <400> 93  
 attgttgatgc aggctgagtt taag 24  
 <210> 94  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
 <400> 94  
 ggtggctata catggatagc aattacctgg acacgctgtc ccggg 45  
 <210> 95  
 <211> 2226  
 <212> DNA  
 <213> Homo sapiens  
 <400> 95  
 agtcgactgc gtccctgtga cccggcgcca gctgtgttcc tgaccccaaga ataactcagg 60  
 gctgcaccgg gctggcagc gctccgcaca catttctgt cgcggcctaa gggaaactgt 120  
 tggccgctgg gcccgcgggg ggattcttgg cagttggggg gtccgctcggg agcgagggcg 180

gaggggaagg gagggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240  
 ccagacacag ctctgcgtcc tcgagcggga cagatccaag ttgggagcag ctctgcgtgc 300  
 ggggcctcag agaattgaggc cggcggttcgc cctgtgcctc ctctggcagg cgctctggcc 360  
 cgggcccgggc ggccggcgaac accccactgc cgaccgtgct ggctgctcgg cctcggggggc 420  
 ctgctacagc ctgcaccacg ctaccatgaa gcggcaggcg gccgaggagg cctgcatect 480  
 gcgaggtggg gcgctcagca ccgtgcgtgc gggcgccgag ctgcgcgctg tgcctgcgct 540  
 cctgcgggca ggcccagggc ccggaggggg ctccaaagac ctgctgttct gggtgcgact 600  
 ggagcgcagg cgttcccact gcaccctgga gaacgagcct ttgcgggggt tctcctggct 660  
 gtctcctcag cccggcggtc tcgaaagcga cacgctgcag tgggtggagg agccccaacg 720  
 ctctgcacc gcgcggagat gcgcggtact ccaggccacc ggtggggtcg agcccgagg 780  
 ctggaaggag atgcgatgcc acctgcgcgc caacggctac ctgtgcaagt accagtttga 840  
 ggtcttgtgt cctgcgcgcg gcccgggggc cgctctaac ttgagctatc gcgcgcctt 900  
 ccagctgcac agcgcgcgctc tggacttcag tccacctggg accgaggtga gtgcgctctg 960  
 ccggggacag ctcccgatct cagttaactg catcgcgagc gaaatcggcg ctgcgtggga 1020  
 caaactctcg ggcgatgtgt tgtgtccctg ccccgggagg tacctcctg ctggcaaagt 1080  
 cgcagagctc cctaactgcc tagacgactt gggaggcttt gcctgcgaat gtgctacggg 1140  
 ctctgagctg gggaaggacg gccgctcttg tgtgaccagt ggggaaggac agccgaccct 1200  
 tggggggacc ggggtgcca ccaggcgccc gccggccact gcaaccagcc ccgtgccgca 1260  
 gagaacatgg ccaatcaggg tcgacgagaa gctgggagag acaccacttg tccctgaaca 1320  
 agacaattca gtaacatcta ttctgagat tctctgatgg ggatcacaga gcacgatgtc 1380  
 tacccttcaa atgtcccttc aagccgagtc aaaggccact atcaccat cagggagcgt 1440  
 gatttccaag tttaattcta cgacttctc tgccactcct caggctttcg actcctctc 1500  
 tgccgtggtc ttcatatttg tgagcacagc agtagtagtg ttggtgatct tgaccatgac 1560  
 agtactgggg cttgtcaagc tctgctttca cgaaagcccc tcttcccagc caaggaagga 1620  
 gtctatgggc ccgcggggcc tggagagtga tcttgagccc gctgctttgg gctccagttc 1680  
 tgcacattgc acaacaatg gggtgaaagt cggggactgt gatctgcggg acagagcaga 1740  
 ggggtgccttg ctggcgaggc cccctcttg ctctagtgt gcataaggaa acagggggaca 1800  
 tgggcactcc tgtgaacagt ttttacttt tgatgaaacg gggaaccaag aggaacttac 1860  
 ttgtgtaact gacaatttct gcagaaatcc ccttctctt aaattccctt tactccactg 1920  
 aggagctaaa tcagaactgc acactccttc cctgatgata gaggaagtgg aagtgccttt 1980  
 aggatgggta tactggggga ccgggtagtg ctggggagag atattttct atgtttattc 2040  
 ggagaatttg gagaagtgt tgaacttttc aagacattgg aaacaaatag aacacaaat 2100  
 aatttacatt aaaaaataat ttctaccaa atggaaagga aatgttctat gttgttcagg 2160  
 ctaggagtat attgggtcga aatcccaggg aaaaaataa aaataaaaaa ttaaaggatt 2220  
 gttgat 2226

<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro  
 1 5 10 15

Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser  
 20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln  
 35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val  
 50 55 60

[illegible]

```
<210> 97
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
```

```
<210> 98
<211> 20
<212> DNA
<213> Artificial Sequence
```

<400>	98	
tgaccagtgg	ggaaggacag	20



<210> 99  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 99  
 acagagcaga gggcgccttg 20  
  
 <210> 100  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 100  
 tcagggacaa gtggtgtctc tccc 24  
  
 <210> 101  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 101  
 tcagggaagg agtgtgcagt tctg 24  
  
 <210> 102  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 102  
 acagctcccg atctcagtta cttgcatcgc ggacgaaatc ggcgctcgct 50  
  
 <210> 103  
 <211> 2026  
 <212> DNA  
 <213> Homo sapiens

<400> 103  
 cggacgcgtg ggattcagca gtggcctgtg gctgccagag cagctcctca ggggaaacta 60  
 agcgtcgagt cagacggcac cataatcgcc tttaaaagtg cctccgccct gccggccgcg 120  
 tatccccggg ctacctgggc cgccccgcgg cggtgcgcgc gtgagagggg gcgcgcgggc 180  
 agccgagcgc cgggtgtgagc cagcgtgtgt gccagtgtga gcggcgggtg gagecgcgtg 240  
 ggtgcggagg ggcgtgtgtg ccggcgcgcg cgccgtgggg tgcaaaccce gagegtctac 300  
 gctgccatga ggggcgcgaa cgccgtgggc ccactctgcc tgetgctggc tgccgccacc 360  
 cagctctcgc ggcagcagtc cccagagaga cctgttttca catgtggtgg cattcttact 420  
 ggagagtctg gattttattg cagtgaaggt ttctctggag tgtaccctcc aaatagcaaa 480  
 tgtacttgga aaatcacagt tcccgaagga aaagtagtgc ttctcaattt ccgattcata 540  
 gacctcgaga gtgacaacct gtgccgctat gactttgtgg atgtgtacaa tggccatgcc 600  
 aatggccagc gcattggccg cttctgtggc actttccggc ctggagccct tgtgtccagt 660  
 ggcaacaaga tgatggtgca gatgatttct gatgccaaaca cagctggcaa tggtttcatg 720  
 gccatgttct ccgctgctga accaaaacgaa agaggggatc agtattgtgg aggactcctt 780  
 gacagacctt ccggtctctt taaaaccccc aactggccag accgggatta ccctgcagga 840  
 gtcacttggt tgtggcacat tgtagcccca aagaatcagc ttatagaatt aaagtttgag 900  
 aagtttgatg tggagcgaga taactactgc cgatatgatt atgtggctgt gtttaattggc 960  
 ggggaagtca acgatgctag aagaattgga aagtattgtg gtgatagtcc acctgcgcca 1020  
 attgtgtctg agagaaatga acttcttatt cagtttttat cagacttaag ttttaactga 1080  
 gatgggttta ttggtcacta catattcagg ccaaaaaaac tgccataaac tacagaacag 1140  
 cctgtcacca ccacattccc tgtaaccacg ggtttaaaac ccaccgtggc cttgtgtcaa 1200  
 caaaagtgtg gacggacggg gactctggag ggcaattatt gttcaagtga ctttgtatta 1260  
 gccggcactg ttatcacaaac catcactcgc gatgggagtt tgcacgccac agtctcgatc 1320  
 atcaacatct acaaagaggg aaatttggcg attcagcagg cgggcaagaa catgagtgcc 1380  
 aggtgactg tegtctgcaa gcagtgcctt ctctcagaa gaggtctaaa ttacattatt 1440  
 atgggccaa taggtgaaga tgggcgaggc aaaatcatgc caaacagctt tatcatgatg 1500  
 ttcaagacca agaatcagaa gctcctggat gccttaaaaa ataagcaatg ttaacagtga 1560  
 actgtgtcca tttaaagctg attctgccat tgcccttgaa agatctatgt tctctcagta 1620  
 gaaaaaaaaa tacttataaa attacatatt ctgaaagagg attccgaaag atgggactgg 1680  
 ttgactcttc acatgatgga ggtatgaggc ctccgagata gctgagggaa gttctttgcc 1740  
 tgctgtcaga ggagcagcta tctgattgga aacctgccga cttagtgcgg tgataggaag 1800  
 ctaaaagtgt caagcgttga cagcttgga gcgtttattt atacatctct gtaaaaggat 1860  
 attttagaat tgagttgtgt gaagatgtca aaaaaagatt ttagaagtgc aatatttata 1920  
 gtgttatttg tttcaccttc aagcctttgc cctgaggtgt tacaatcttg tcttgcgttt 1980  
 tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa 2026

<210> 104  
 <211> 415  
 <212> PRT  
 <213> Homo sapiens

<400> 104  
 Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala  
 1 5 10 15  
 Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr  
 20 25 30  
 Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly  
 35 40 45  
 Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr  
 50 55 60

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu  
 65 70 75 80  
 Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly  
 85 90 95  
 His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro  
 100 105 110  
 Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser  
 115 120 125  
 Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala  
 130 135 140  
 Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg  
 145 150 155 160  
 Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro  
 165 170 175  
 Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu  
 180 185 190  
 Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys  
 195 200 205  
 Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala  
 210 215 220  
 Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val  
 225 230 235 240  
 Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu  
 245 250 255  
 Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu  
 260 265 270  
 Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr  
 275 280 285  
 Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr  
 290 295 300  
 Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly  
 305 310 315 320  
 Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val  
 325 330 335  
 Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100

[illegible]

<212> DNA

<213> Homo sapiens

<400> 108

cggacgcgtg ggcggacgcg tgggcggccc acggcgcccc cgggctgggg cggtcgcttc 60  
 ttcccttctcc gtggcctacg aggggtcccca gcctgggtaa agatggcccc atggcccccg 120  
 aagggcctag tcccagctgt gctctggggc ctcagcctct tcctcaacct cccaggacct 180  
 atctggctcc agccctctcc acctccccag tcttctcccc cgcttcagcc ccatccgtgt 240  
 catacctgcc ggggactggg tgacagcttt aacaagggcc tggagagAAC catccgggac 300  
 aactttggag gtggaaacac tgcttgggag gaagagaatt tgtccaaata caaagacagt 360  
 gagaccgcgc tggtagagggt gctggagggt gtgtgcagca agtcagactt cgagtgccac 420  
 cgcttgcctg agctgagtga ggagctgggt gagagctggg ggtttcacaa gcagcaggag 480  
 gccccggacc tcttccagtg gctgtgctca gattccctga agctctgctg ccccgagggc 540  
 accttcggggc cctcctgcct tccctgtcct gggggaaacag agaggccctg cggtggctac 600  
 gggcagtgtg aaggagaagg gacacgaggg ggcagcgggc actgtgactg ccaagccggc 660  
 tacgggggtg aggcctgtgg ccagtgtggc cttggctact ttgaggcaga acgcaacgcc 720  
 agccatctgg tatgttcggc ttgttttggc cctgtgccc gatgctcagg acctgaggaa 780  
 tcaaaactgt tgcaatgcaa gaagggtgtg gccctgcac acctcaagtg tgtagacatt 840  
 gatgagtgtg gcacagaggg agccaactgt ggagctgacc aattctgcgt gaacactgag 900  
 ggctcctatg agtgccgaga ctgtgccaag gcctgcctag gctgcatggg ggcagggcca 960  
 ggtcgctgta agaagtgtag cctgggctat cagcagggtg gctccaagtg tctcgatgtg 1020  
 gatgagtgtg agacagagggt gtgtccggga gagaacaagc agtgtgaaaa caccgagggc 1080  
 ggttatcgct gcatctgtgc cgagggtac aagcagatgg aaggcatctg tgtgaaggag 1140  
 cagatcccag agtcagcagg cttcttctca gagatgacag aagacgagtt ggtgggtgctg 1200  
 cagcagatgt tctttggcat catcatctgt gcaactggcca cgctggctgc taaggcgac 1260  
 ttggtgttca ccgccatctt cattggggct gtggcgcca tgactggcta ctggttgtca 1320  
 gagcgcagtg accgtgtgct ggagggttc atcaaggcca gataatcgcg gccaccacct 1380  
 gtaggacctc ctcccacca cgctgcccc agagcttggg ctgcccctct gctggacact 1440  
 caggacagct tgggttattt ttgagagtgg ggtaagcacc cctacctgcc ttacagagca 1500  
 gcccaggtag ccaggccccg gcagacaagg cccctggggg aaaaagtagc cctgaagggtg 1560  
 gataccatga gctcttcacc tggcggggac tggcaggctt cacaatgtgt gaatttcaaa 1620  
 agtttttctt taatggtggc tgctagagct ttggccctg cttaggatta ggtggtcctc 1680  
 acaggggtgg ggccatcaca gctccctct gccagctgca tgetgccagt tctgttctg 1740  
 tgttcaccac atccccacac cccattgcca cttatttatt catctcagga aataaagaaa 1800  
 ggtcttgtaa agttaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly  
 1 5 10 15  
 Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser  
 20 25 30  
 Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr  
 35 40 45  
 Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile  
 50 55 60

For "Seq" show

Arg 65	Asp	Asn	Phe	Gly	Gly 70	Gly	Asn	Thr	Ala	Trp 75	Glu	Glu	Glu	Asn	Leu 80
Ser	Lys	Tyr	Lys	Asp 85	Ser	Glu	Thr	Arg	Leu 90	Val	Glu	Val	Leu	Glu 95	Gly
Val	Cys	Ser	Lys 100	Ser	Asp	Phe	Glu	Cys 105	His	Arg	Leu	Leu	Glu 110	Leu	Ser
Glu	Glu	Leu 115	Val	Glu	Ser	Trp	Trp 120	Phe	His	Lys	Gln	Gln 125	Glu	Ala	Pro
Asp	Leu 130	Phe	Gln	Trp	Leu	Cys 135	Ser	Asp	Ser	Leu	Lys 140	Leu	Cys	Cys	Pro
Ala 145	Gly	Thr	Phe	Gly	Pro 150	Ser	Cys	Leu	Pro	Cys 155	Pro	Gly	Gly	Thr	Glu 160
Arg	Pro	Cys	Gly	Gly 165	Tyr	Gly	Gln	Cys	Glu 170	Gly	Glu	Gly	Thr	Arg 175	Gly
Gly	Ser	Gly	His 180	Cys	Asp	Cys	Gln	Ala 185	Gly	Tyr	Gly	Gly	Glu 190	Ala	Cys
Gly	Gln 195	Cys	Gly	Leu	Gly	Tyr	Phe 200	Glu	Ala	Glu	Arg	Asn 205	Ala	Ser	His
Leu 210	Val	Cys	Ser	Ala	Cys	Phe 215	Gly	Pro	Cys	Ala	Arg 220	Cys	Ser	Gly	Pro
Glu 225	Glu	Ser	Asn	Cys	Leu 230	Gln	Cys	Lys	Lys	Gly 235	Trp	Ala	Leu	His	His 240
Leu	Lys	Cys	Val	Asp 245	Ile	Asp	Glu	Cys	Gly 250	Thr	Glu	Gly	Ala	Asn 255	Cys
Gly	Ala	Asp	Gln 260	Phe	Cys	Val	Asn	Thr 265	Glu	Gly	Ser	Tyr	Glu 270	Cys	Arg
Asp	Cys 275	Ala	Lys	Ala	Cys	Leu	Gly 280	Cys	Met	Gly	Ala	Gly 285	Pro	Gly	Arg
Cys	Lys 290	Lys	Cys	Ser	Pro	Gly 295	Tyr	Gln	Gln	Val	Gly 300	Ser	Lys	Cys	Leu
Asp 305	Val	Asp	Glu	Cys	Glu 310	Thr	Glu	Val	Cys	Pro 315	Gly	Glu	Asn	Lys	Gln 320
Cys	Glu	Asn	Thr	Glu 325	Gly	Gly	Tyr	Arg	Cys 330	Ile	Cys	Ala	Glu	Gly 335	Tyr
Lys	Gln	Met	Glu 340	Gly	Ile	Cys	Val	Lys 345	Glu	Gln	Ile	Pro	Glu 350	Ser	Ala

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
 355 360 365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
 385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
 405 410 415

Ile Lys Gly Arg  
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga 50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc 22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac 22

<210> 113

<211> 1616  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1461)  
 <223> a, t, c or g

<400> 113  
 tgagaccctc ctgcagcctt ctcaagggac agccccactc tgcctcttgc tectccaggg 60  
 cagcaccatg cagccccctgt ggctctgctg ggcactctgg gtgttgcccc tggccagccc 120  
 cggggccgcc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180  
 agaggtgccc accctggaca gggccgacat ggaggagctg gtcaccccca cccacgtgag 240  
 ggcccagtac gtggccctgc tgcagcgcag ccacggggac cgctcccgcg gaaagaggtt 300  
 cagccagagc ttccgagagg tggccggcag gttcctggcg ttggaggcca gcacacacct 360  
 gctggtgttc ggcattggagc agcggctgcc gcccaacagc gagctggtgc agggcgtgct 420  
 gcggctcttc caggagccgg tccccaaagg ccgcgtgcac aggcacgggc ggctgtcccc 480  
 gcgcagcgcc cggggccggg tgaccgtcga gtggctgcgc gtccgcgacg acggctccaa 540  
 ccgcacctcc ctcatcgact ccaggctggt gtccgtccac gagagcggct ggaaggcctt 600  
 cgagctgacc gaggcctgga acttctggca gcagctgagc cggccccggc agcgcgtgct 660  
 gctacagggtg tcggtgcaga gggagcatct gggcccgctg gcgtccggcg cccacaagct 720  
 ggctccgcttt gcctcgcagg gggcgccagc cgggcttggg gagccccagc tggagctgca 780  
 caccctggac cttggggact atggagctca gggcgactgt gacctgaag caccaatgac 840  
 cgagggcacc cgctgctgcc gccaggagat gtacattgac ctgcagggga tgaagtgggc 900  
 cgagaactgg gtgctggagc ccccgggctt cctggcttat gagtgtgtgg gcacctgccg 960  
 gcagcccccg gaggccttg ccttcaagtg gccgtttctg gggcctcgac agtgcctgcg 1020  
 ctcgagact gactcgctgc ccatgatcgt cagcatcaag gagggaggca ggaccaggcc 1080  
 ccagggtggtc agcctgccc acatgagggt gcagaagtgc agctgtgctt cggatggtgc 1140  
 gctcgtgcca aggaggtcc agccataggc gcctagtgtg gccatcgagg gacttgactt 1200  
 gtgtgtgttt ctgaagtgtt cgaggggtacc aggagagctg gcgatgactg aactgctgat 1260  
 ggacaaatgc tctgtgctct ctagtgagcc ctgaatttgc ttctctgac aagttacctc 1320  
 acctaatttt tgcttctcag gaatgagaat ctttggccac tggagagccc ttgctcagtt 1380  
 ttctctattc ttattattca ctgcactata ttctaagcac ttacatgtgg agatactgta 1440  
 acctgagggc agaaagccca ntgtgtcatt gtttacttgt cctgtcactg gatctgggct 1500  
 aaagtctccc accaccactc tggacctaa acctgggggt aagtgtgggt tgtgcatccc 1560  
 caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

<210> 114  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
 Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala  
 1 5 10 15  
 Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu  
 20 25 30  
 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
 35 40 45

104120 3304000



Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
 50 55 60  
 Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln  
 65 70 75 80  
 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
 85 90 95  
 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
 100 105 110  
 Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
 115 120 125  
 Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg  
 130 135 140  
 Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr  
 145 150 155 160  
 Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys  
 165 170 175  
 Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg  
 180 185 190  
 Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu  
 195 200 205  
 Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln  
 210 215 220  
 Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu  
 225 230 235 240  
 Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro  
 245 250 255  
 Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu  
 260 265 270  
 Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe  
 275 280 285  
 Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu  
 290 295 300  
 Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu  
 305 310 315 320  
 Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr  
 325 330 335

100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser  
                   340                  345                  350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
                   355                  360                  365

<210> 115  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 115  
 aggactgcc a taactgcct g 21

<210> 116  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 116  
 ataggagttg aagcagcgct gc 22

<210> 117  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 117  
 tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc 45

<210> 118  
 <211> 1857  
 <212> DNA  
 <213> Homo sapiens

<400> 118  
 gtctgttccc aggagtcctt cggcggctgt tgtgtcagtg gctgatcgc gatggggaca 60  
 aaggcgcaag tcgagaggaa actgttgtgc ctcttcata tggcgatcct gttgtgctcc 120  
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 180

CCDS:CCDS10000.1

aatcctgtga agttgtcctg tgcctactcg ggctttttctt ctccccgtgt ggagtgggaag 240  
tttgaccaag gagacaccac cagactcggt tgcctataata acaagatcac agcttcctat 300  
gaggaccggg tgaccttctt gccaaactggt atcaccttca agtccgtgac acgggaagac 360  
actgggacat acacttgat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420  
gtcaagctca tctgtcttgt gcctccatcc aagcctacag ttaacatccc ctctctgcc 480  
accattggga accgggcagt gctgacatgc tcagaacaag atgggtcccc acctctgaa 540  
tacacctggt tcaaagatgg gatagtgat cctacgaatc ccaaaagcac cctgaccttc 600  
agcaactctt cctatgtcct gaatcccaca acaggagagc tgggtcttga tccctgtca 660  
gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720  
tcaaagtctg tgcgcattga agctgtggag cgggaatgtg gggatcatcg ggcagccgtc 780  
cttghtaacc tgattctcct gggaatcttg gtttttgcca tctgggttgc ctatagccga 840  
ggccactttg acagaacaaa gaaagggact tgcagtaaga aggtgattta cagccagcct 900  
agtccccgaa gtgaaggaga attcaaacag aactcgatcat tctgggtgtg agcctgggtcg 960  
gctcacgcgc tatcatctgc atttgcctta ctccaggtgct accggactct ggccccgat 1020  
gtctgtagtt tcacaggatg ccttatttgt cttctacacc ccacagggcc cctacttct 1080  
tcggatgtgt ttttaataat gtcagctatg tgcctccatcc tcttcatgc cctccctccc 1140  
tttctacca ctgctgagtg gcctggaact tgtttaaagt gtttattccc catttctttg 1200  
agggatcagg aaggaatcct gggatgcca ttgacttccc ttctaagtag acagcaaaaa 1260  
tggcgggggt cgcaggaatc tgcactcaac tgcctccctg gctggcaggg atctttgaat 1320  
aggtatcttg agcttggttc tgggctctt ccttgtgtac tgacgaccag ggcagctgt 1380  
tctagagcgg gaattagagg ctagagcggc tgaaatgggt gtttgggtgat gacactggg 1440  
tccttccatc tctggggccc actctcttct gtcttcccat gggagtgcc actgggatcc 1500  
ctctgccctg tctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaatggg 1560  
agctcttgtt gtggagagca tagtaaat ttcagagaact tgaagccaaa aggatttaaa 1620  
accgctgctc taaagaaaag aaaactggag gctgggcgca gtggctcacg cctgtaatcc 1680  
cagaggctga ggcaggcgga tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740  
ggagaaaccc tactggaaat acaaagttag ccaggcatgg tgggtcatgc ctgtagtccc 1800  
agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa aaaaaaa 1857

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile  
1 5 10 15

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
85 90 95





## oligonucleotide probe

&lt;400&gt; 125

actcagcagt ggtaggaaag

20

&lt;210&gt; 126

&lt;211&gt; 1210

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 126

```

cagcgcgtgg cgggcgcgcg tgtgggggaca gcatgagcgg cggttggatg ggcaggttg 60
gagcgtggcg aacaggggct ctgggcctgg cgtgctgct gctgctcggc ctgggactag 120
gcctggaggc cgcgcgcgag ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180
gctcaggctc gtgcccaccc accaagttcc agtgcgcgac cagtggctta tgcgtgcccc 240
tcacctggcg ctgcgcagag gacttggact gcagcgatgg cagcgatgag gaggagtga 300
ggattgagcc atgtaccag aaagggcaat gcccaccgcc cctggcctc cctgccccct 360
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420
tggcctgcct agcaggcgag ctccgttgca cgtgagcga tgactgcatt ccactcacgt 480
ggcgtgcga cgccaccca gactgtccc actccagcga cgagctcggc tgtggaacca 540
atgagatcct ccggaaggg gatgccacaa ccatggggcc cctgtgacc ctggagagt 600
tcacctctct caggaatgcc acaaccatgg ggccccctgt gacctggag agtgtcccc 660
ctgtcgggaa tgcacatcc tctctgccg gagaccagtc tggaaagcca actgcctatg 720
gggttattgc agctgctgcg gtgctcagt caagcctgg caccgccacc ctctctctt 780
tgtcctggct ccgagcccag ggcgcctcc gccactggg gttactggtg gccatgaagg 840
agtccttgc gctgtcagaa cagaagacct cgtgccctg aggacaagca cttgccacca 900
ccgtcactca gccctgggcg tagccggaca ggaggagagc agtgatgcgg atgggtaccc 960
gggcacacca gccctcagag acctgagttc ttctggccac gtggaacctc gaaccgcagc 1020
tctgcagaa gtggccctgg agattgaggg tccctggaca ctccctatgg agatccgggg 1080
agctaggatg gggaaacctgc cacagccaga actgaggggc tggcccagc cagctcccag 1140
ggggtagaac ggccctgtgc ttaagacact cctgctgcc ccgtctgagg gtggcgatta 1200
aagttgcttc                                     1210

```

&lt;210&gt; 127

&lt;211&gt; 282

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 127

```

Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
  1             5             10             15

```

```

Leu Gly Leu Ala Leu Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
      20             25             30

```

```

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
    35             40             45

```

```

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
    50             55             60

```

```

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
    65             70             75             80

```

F04F20-9540500

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln  
                             85                            90                            95  
 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly  
                             100                            105                            110  
 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser  
                             115                            120                            125  
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp  
                             130                            135                            140  
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp  
                             145                            150                            155                            160  
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly  
                             165                            170                            175  
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser  
                             180                            185                            190  
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val  
                             195                            200                            205  
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly  
                             210                            215                            220  
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala  
                             225                            230                            235                            240  
 Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln  
                             245                            250                            255  
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu  
                             260                            265                            270  
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro  
                             275                            280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

<210> 129

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 129

ttggttccac agccgagctc gtcg

24

<210> 130

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 130

gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc

50

<210> 131

<211> 1843

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (1837)

<223> a, t, c or g

<400> 131

```

cccacgcgtc cgggtctcgtc cgctcgcgca gcggcggcag cagaggtcgc gcacagatgc 60
gggttagact ggcgggggga ggaggcggag gaggggaagg agctgcatgc atgagaccca 120
cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccga 180
gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
gactcttggc cgtgatcctg tggtttcagc tggcgctgtg ctteggccct gcacagctca 300
cgggcggggt cgatgacett caagtgtgtg ctgaccccg gattccccag aatggcttca 360
ggacccccag cggagggggt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420
gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480
gctggatccc aagtataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatcg 540
aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgct 600
atgaaggatt caagatccgg taccgcgacc tacacaatat ggtttcatta tgcgcgatg 660
atggaacgtg gaataatctg cccatctgtc aaggtgcct gagacctcta gcctcttcta 720
atggctatgt aaacatctct gagctccaga cctcctccc ggtggggact gtgatctcct 780
atcgtgctt tcccggattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840
ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900
ctccaatggt gagtcacgga gatttcgtct gccaccgcg gccttgtagc cgctacaacc 960
acggaactgt ggtggagttt tactgcgatc ctggctacag cctcaccagc gactacaagt 1020
acatcacctg ccagtatgga gagtgggttc cttcttatca agtctactgc atcaaatcag 1080
agcaaactg gccagcacc catgagaccc tcttgaccac gtggaagatt gtggcggttca 1140

```

40420 3364060



cggcaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200  
 agttcaaggc ccactttccc cccagggggc ctccccggag ttccagcagt gaccctgact 1260  
 ttgtgggtgt agacggcgtg cccgtcatgc tcccgtccta tgacgaagct gtgagtggcg 1320  
 gcttgagtgc cttaggcccc gggtacatgg cctctgtggg ccagggtgc cccttaccg 1380  
 tggacgacca gagccccca gcataccccg gctcagggga cacggacaca ggcccagggg 1440  
 agtcagaaac ctgtgacagc gtctcaggct cttctgagct gctccaaagt ctgtattcac 1500  
 ctcccagggtg ccaagagagc acccacctg ctccggacaa ccctgacata attgccagca 1560  
 cggcagagga ggtggcatcc accagcccag gcattccatca tgcccactgg gtgttggtcc 1620  
 taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680  
 gttgatctgt ggagttgatt cctttccttc tcttggtttt agacaaatgt aaacaaagct 1740  
 ctgatcctta aaattgctat gctgatagag tggtaggggc tggaagcttg atcaagtctt 1800  
 gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln  
 1 5 10 15

Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val  
 20 25 30

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr  
 35 40 45

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu  
 50 55 60

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val  
 65 70 75 80

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys  
 85 90 95

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser  
 100 105 110

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu  
 115 120 125

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile  
 130 135 140

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn  
 145 150 155 160

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile  
 165 170 175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

104720"93640650

180	185	190
Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr 195 200 205		
Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys 210 215 220		
Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu 225 230 235 240		
Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe 245 250 255		
Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val 260 265 270		
Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr 275 280 285		
Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys 290 295 300		
Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr 305 310 315 320		
Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu 325 330 335		
Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His 340 345 350		
Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe 355 360 365		
Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala 370 375 380		
Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val 385 390 395 400		
Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr 405 410 415		
Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys 420 425 430		
Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro 435 440 445		
Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile 450 455 460		

180 185 190  
 195 200 205  
 210 215 220  
 225 230 235 240  
 245 250 255  
 260 265 270  
 275 280 285  
 290 295 300  
 305 310 315 320  
 325 330 335  
 340 345 350  
 355 360 365  
 370 375 380  
 385 390 395 400  
 405 410 415  
 420 425 430  
 435 440 445  
 450 455 460

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn  
 485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 133

atctcctatc gctgctttcc cgg

23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc

23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 135

atttaaactt gatgggtctg cgtatcttga gtgcttaca aaccttatct

50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

cccacgcgtc cgctccgcgc cctccccccc gcctcccgtg cggtcgcgtc gtggcctaga 60  
 gatgctgctg ccgcgggtgc agttgtcgcg cagcctctg cccgccagcc cgctccaccg 120  
 ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180  
 tacaggccgt gctgctggcc gtgctgctgg tggggtgcg ggccgcgacg ggtcgctgc 240  
 tgagtgcctc ggatttggac ctcagaggag ggcagccagt ctgccgggga gggacacaga 300

ggccttggtta taaagtcatt tacttccatg atactttctcg aagactgaac tttgaggaag 360  
 ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtc gaagatgaac 420  
 agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatggtgac ttctggattg 480  
 ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540  
 ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tectgcgcca 600  
 gcgaggtctg cgtgggtcatg taccatcagc catcggcacc cgctggcatc ggaggccctt 660  
 acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaatatt 720  
 ctgatgagaa accagcagtt cttctagag aagctgaagg tgaggaaaca gagctgacaa 780  
 cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840  
 gagaagctgc cttgaatctg gcctacatcc taatccccag cattccccctt ctctctctcc 900  
 ttgtgggtcac cacagttgta tgttgggtt ggatctgtag aaaaagaaaa cgggagcagc 960  
 cagaccctag cacaagaag caacacacca tctggccctc tctcaccag ggaaacagcc 1020  
 cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagacc 1080  
 ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140  
 tgtcttgtga ctatgacaac atggctgtga acccatcaga aagtgggtt gtgactctgg 1200  
 tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca gaccaaattg 1260  
 ggaggagtaa ggagtcgtga tgggtggaaa atgaaatata tgggtattag gacataaaa 1320  
 aaactgaaac tgacaacaat ggaaaagaaa tgataagcaa aatcctctta tttctataa 1380  
 ggaaaataca cagaaggtct atgaacaagc ttagatcagg tctgtggat gagcatgtgg 1440  
 tccccacgac ctctgttg accccacgt tttggctgta tcttttatcc cagccagtca 1500  
 tccagctcga cttatgaga aggtacctg cccaggtctg gcacatagta gagtctcaat 1560  
 aaatgtcact tggttggttg tatctaactt ttaagggaca gagctttacc tggcagtgat 1620  
 aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680  
 atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740  
 ttggcctgtg catcggaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800  
 agcaggaaaa aaaaa 1815

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu  
1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser  
65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
100 105 110

<210> 138

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 140  
 cagtccaagc ataaagggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
 gcatccgcag gttcccgagg acttgggggc gcccgctgag ccccggcgcc cgcagaagac 120  
 ttgtgtttgc ctctgcagc ctcaaccggg agggcagcga gggcctacca ccatgatcac 180  
 tgggtgtgttc agcatgcgct tgtggacccc agtgggcgct ctgacctcgc tggcgtactg 240  
 cctgcaccag cggcgggtgg ccctggccga gctgcaggag gccgatggcc agtgtccggg 300  
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggctcgtg ttccgacacg gggctcggag 360  
 tcctctcaag ccgctcccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420  
 cccaccccaa actcagtttg attacacagt caccaatcta gctggtgggc cgaaaccata 480  
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540  
 gctgaccaag gtgggcatgc agcaaagtgt tgccctggga gagagactga ggaagaacta 600  
 tgtggaagac attccctttc ttccaccaac cttcaacca caggaggtct ttattcgttc 660  
 cactaacatt ttccggaatc tggagtccac ccgttggttg ctggctgggc ttttccagtg 720



Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His  
 180 185 190  
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
 195 200 205  
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
 210 215 220  
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
 225 230 235 240  
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
 245 250 255  
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
 260 265 270  
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
 275 280 285  
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
 290 295 300  
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
 305 310 315 320  
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
 325 330 335  
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
 340 345 350  
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
 355 360 365  
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
 370 375 380  
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
 385 390 395 400  
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
 405 410 415  
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
 420 425

&lt;210&gt; 143

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

P04720-95610600



<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 144

gcagctctat taccacggga agga

24

<210> 145

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 145

tccttcccgt ggtaatagag ctgc

24

<210> 146

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 146

ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg

45

<210> 147

<211> 1686

<212> DNA

<213> Homo sapiens

<400> 147

ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60  
cttaaatttc agctcatcac cttcacctgc cttgggtcatg gctctgctat tctccttgat 120  
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240  
 gtgtgatgac ggctgggaca ttaaggacgt ggctgtgttg tgccgggagc tgggctgtgg 300  
 agctgccagc ggaaccccta gtggtathtt gtatgagcca ccagcagaaa aagagcaaaa 360  
 ggtoctcatc caatcagtca gttgcacagg aacagaagat acattggctc agtgtgagca 420  
 agaagaagtt tatgattggt cacatgatga agatgctggg gcatcgtgtg agaaccaga 480  
 gagctctttc tccccagtcc cagagggtgt caggctggct gacggccctg ggcattgcaa 540  
 gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600  
 cctccggggc gcaaagggtg tgtgccggca gctgggatgt gggagggtg tactgactca 660  
 aaaacgctgc aacaagcatg cctatggccg aaaacccatc tggctgagcc agatgtcatg 720  
 ctccaggacga gaagcaacc ttcaggattg ccttcttggg ccttggggga agaacacctg 780  
 caacatgat gaagacacgt gggtcgaatg tgaagatccc tttgacttga gactagtagg 840  
 aggagacaac ctctgctctg ggcgactgga ggtgctgcac aagggcgtat ggggctctgt 900  
 ctgtgatgac aactggggag aaaaggagga ccagggtgta tgcaagcaac tgggctgtgg 960  
 gaagtccctc tctccctcct tcagagaccg gaaatgctat ggccctgggg ttggccgcat 1020  
 ctggctggat aatgttctgt gctcagggga ggagcagtc ctggagcagt gccagcacag 1080  
 attttggggg tttcacgact gcacccacca ggaagatgtg gctgtcatct gctcagtgtg 1140  
 ggtgggcatc atctaactg ttgagtgcct gaatagaaga aaaacacaga agaaggaggc 1200  
 atttactgtc tacatgactg catgggatga acactgatct tcttctgccc ttggactggg 1260  
 acttatactt ggtgcccctg attctcaggc cttcagagtt ggatcagaac ttacaacatc 1320  
 aggtctagtt ctccaggccat cagacatagt ttggaactac atcaccacct ttcctatgtc 1380  
 tccacattgc acacagcaga tccccagcct ccataattgt gtgtatcaac tacttaaata 1440  
 cattctcaca cacacacaca cacacacaca cacacacaca cacacataca ccatttgtcc 1500  
 tgtttctctg aagaactctg acaaaataca gattttggta ctgaaagaga ttctagagga 1560  
 acggaathtt aaggataaat tttctgaatt gggttatggg tttctgaaat tggctctata 1620  
 atctaattag atataaaatt ctggttaact tatttacaat aataaagata gcactatgtg 1680  
 ttcaaa 1686

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly  
 1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg  
 20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val  
 35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu  
 50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu  
 65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys  
 85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr  
 100 105 110

000495 9540660

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu  
 115 120 125  
 Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro  
 130 135 140  
 Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr  
 145 150 155 160  
 Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys  
 165 170 175  
 Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn  
 180 185 190  
 Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys  
 195 200 205  
 Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly  
 210 215 220  
 Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp  
 225 230 235 240  
 Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg  
 245 250 255  
 Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn  
 260 265 270  
 Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly  
 275 280 285  
 Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly  
 290 295 300  
 Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln  
 305 310 315 320  
 Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr  
 325 330 335  
 His Gln Glu Asp Val Ala Val Ile Cys Ser Val  
 340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

&lt;400&gt; 149

ttcagctcat caccttcacc tgcc

24

&lt;210&gt; 150

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 150

ggctcataca aaataccact aggg

24

&lt;210&gt; 151

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 151

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt

50

&lt;210&gt; 152

&lt;211&gt; 1427

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 152

actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctcgacctcg 60  
 acccaecgt ccgcggacgc gtgggcggac gcgtgggccc gctaccagga agagtctgcc 120  
 gaagggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tggctcggctg 180  
 cctgggcgtc ttcggcctct tccggctgct gcagtgggtg cgcgggaagg cctacctgcg 240  
 gaatgctgtg gtggtgatca caggcgccac ctcagggtcg ggcaaagaat gtgcaaaagt 300  
 cttctatgct gcgggtgcta aactggtgct ctgtggcccg aatggtgggg ccctagaaga 360  
 gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420  
 ggtgaccttc gacctcacag actctggggc catagttgca gcagcagctg agatcctgca 480  
 gtgctttggc tatgtcgaca tacttgtcaa caatgctggg atcagctacc gtggtaccat 540  
 catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600  
 tgcctaacg aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgc 660  
 catcagcagc atccagggca agatgagcat tccttttcga tcagcatatg cagcctccaa 720  
 gcacgcaacc caggctttct ttgactgtct gcgtggccgag atggaacagt atgaaattga 780  
 ggtgaccgtc atcagccccg gctacatcca caccaacctc tctgtaaatg ccatcaccgc 840  
 ggatggatct aggtatggag ttatggacac caccacagcc caggggccgaa gccctgtgga 900  
 ggtggcccag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960  
 cttactgect tccttggtcg tttatcttcg aactctggct cctgggctct tcttcagcct 1020  
 catggcctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080

```
<210> 153
<211> 310
<212> PRT
<213> Homo sapiens
```

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys  
1 5 10 15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys  
20 25 30

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly  
35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu  
50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu  
65 70 75 80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu  
85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala  
100 105 110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala  
115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp  
130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys  
145 150 155 160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala  
165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr  
180 185 190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala  
195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

210                                      215                                      220  
 Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg  
 225                                      230                                      235                                      240  
 Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu  
                                     245                                      250                                      255  
 Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val  
                                     260                                      265                                      270  
 Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu  
                                     275                                      280                                      285  
 Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu  
                                     290                                      295                                      300

Arg Lys Ser Lys Asn Ser  
 305                                      310

<210> 154  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                                     oligonucleotide probe

<400> 154  
 ggtgctaaac tgggtgctctg tggc

24

<210> 155  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                                     oligonucleotide probe

<400> 155  
 cagggcaaga tgagcattcc

20

<210> 156  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                                     oligonucleotide probe

"GAG" sequence

<400> 156  
tcatactggtt ccatactcggc acgc 24

<210> 157  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 157  
aatggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc 50

<210> 158  
<211> 1771  
<212> DNA  
<213> Homo sapiens

<400> 158  
cccacgcgtc cgctgggtgtt agatcgagca accctctaaa agcagtttag agtggtaaaa 60  
aaaaaaaaaa acacacccaaa cgctcgcagc cacaaaaggg atgaaatttc ttctggacat 120  
cctcctgctt ctcctgttac tgatcgtctg ctccttagag tccttcgtga agctttttat 180  
tcctaagagg agaaaatcag tcaccggcga aatcgtgctg attacaggag ctgggcatgg 240  
aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300  
tataaataag catggactgg aggaaacagc tgccaaatgc aagggaactgg gtgccaaggt 360  
tcataccttt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaaggt 420  
gaaggcagaa attggagatg ttagtatttt agtaataat gctggtgtag tctatacatc 480  
agatttgttt gctacacaag atcctcagat tgaaaagact tttgaagtta atgtacttgc 540  
acatttctgg actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600  
tgtcaactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg cttactgttc 660  
aagcaagttt gctgctgttg gatctcataa aactttgaca gatgaactgg ctgccttaca 720  
aataactgga gtcaaaaacaa catgtctgtg tcttaatttc gtaaacactg gcttcatcaa 780  
aaatccaagt acaagtttgg gacccactct ggaacctgag gaagtggtaa acaggctgat 840  
gcatgggatt ctgactgagc agaagatgat ttttattcca tcttctatag cttttttaac 900  
aacattggaa aggatccttc ctgagcgttt cctggcagtt ttaaaacgaa aaatcagtgt 960  
taagtttgat gcagttattg gatataaaat gaaagcgcaa taagcaccta gttttctgaa 1020  
aactgattta ccaggtttag gttgatgtca tctaatagtg ccagaatttt aatgtttgaa 1080  
cttctgtttt ttctaattat cccattttct tcaatatcat ttttgaggct ttggcagttc 1140  
tcatttacta ccacttgttc tttagccaaa agctgattac atatgatata aacagagaaa 1200  
taccttttaga ggtgacttta aggaaaatga agaaaaagaa ccaaaatgac tttattaaaa 1260  
taatttccaa gattatttgt ggctcacctg aaggctttgc aaaatttgta ccataaccgt 1320  
ttattttaaca tatattttta tttttgattg cacttaaatt ttgtataatt tgtgtttctt 1380  
tttctgttct acataaaatc agaaacttca agctctctaa ataaaatgaa ggactatatc 1440  
tagtggtatt tcacaatgaa tatcatgaac tctcaatggg taggtttcat cctaccatt 1500  
gccactctgt ttcttgagag atacctcaca ttccaatgcc aaacatttct gcacagggaa 1560  
gctagaggtg gatcacgtg ttgcaagtat aaaagcatca ctgggattta aggagaattg 1620  
agagaatgta cccacaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaa 1680  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a a 1771

<210> 159





Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile  
260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys  
275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln  
290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 161

atcccatgca tcagcctggt tacc

24

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 162

gctggtgtag tctatacatc agatttggtt gctacacaag atcctcag

48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

cccacgcgtc cgcggacgcg tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60  
tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaaggtg 120

attgttttcg tggtcctgtt gatgcctggc cctgtgatg ggctgttttcg ctccctatac 180  
 agaagtgttt ccatgccacc taaggggagac tcaggacagc cattattttct caccctttac 240  
 attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggtcggccc tttcccagga 300  
 ctgaacatga agagttatgc cggttctctc accgtgaata agacttataa cagcaacctc 360  
 ttcttctggt tcttcccagc tcagatacag ccagaagatg cccagtagt tctctggcta 420  
 caggggtggc cgggaggttc atccatgttt ggactctttg tggacatggt gccttatgtt 480  
 gtcacaagta acatgacctt gcgtgacaga gacttcccct ggaccacaac gctctccatg 540  
 ctttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600  
 gcagtcaatg aggacgatgt agcacgggat ttatacagt cactaattca gtttttccag 660  
 atatttctctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720  
 tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780  
 aacctgaacg gaattgctat tggagatgga tattctgatc ccgaatcaat tatagggggc 840  
 tatgcagaat tctgtacca aattggcttg ttggatgaga agcaaaaaaaaa gtacttccag 900  
 aagcagtgcc atgaatgcat agaacacatc aggaagcaga actgggtttga ggcttttgaa 960  
 atactggata aactactaga tggcgactta acaagtgatc cttcttactt ccagaatgtt 1020  
 acaggatgta gtaattacta taactttttg cggtgcacgg aacctgagga tcagctttac 1080  
 tatgtgaaat tttgtcact cccagaggtg agacaagcca tccacgtggg gaatcagact 1140  
 tttaatgatg gaactatagt tgaaaagtac ttgcgagaag atacagtaca gtcagttaag 1200  
 ccattggttaa ctgaaatcat gaataattat aaggttctga tctacaatgg ccaactggac 1260  
 atcatcgtgg cagctgcctt gacagagcgc tccttgatgg gcatggactg gaaaggatcc 1320  
 caggaatata agaaggcaga aaaaaaagt ttggaagatct ttaaatctga cagtgaagtg 1380  
 gctggttaca tccggcaagc gggtgacttc catcaggtaa ttattcgagg tggaggacat 1440  
 attttacctt atgaccagcc tctgagagct tttgacatga ttaatcgatt catttatgga 1500  
 aaaggatggg atccttatgt tggataaaact accttcccaa aagagaacat cagaggtttt 1560  
 cattgctgaa aagaaaatcg taaaaacaga aaatgtcata ggaataaaaa aattatcttt 1620  
 tcatatctgc aagatttttt tcatcaataa aaattatcct tgaaacaagt gagcttttgt 1680  
 ttttgggggg agatgtttac tacaaaatta acatgagtag atgagtaaga attacattat 1740  
 ttaacttaaa ggatgaaagg tatggatgat gtgacactga gacaagatgt ataaatgaaa 1800  
 ttttagggtc ttgaatagga agtttttaatt tcttctaaga gtaagtgaaa agtgcagttg 1860  
 taacaaacaa agctgtaaca tctttttctg ccaataacag aagtttggca tgccgtgaag 1920  
 gtgtttggaa atattattgg ataagaatag ctcaattatc ccaataaaat ggatgaagct 1980  
 ataatagttt tggggaaaaag attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040  
 gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met  
 1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser  
 20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr  
 35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly  
 50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

for 20' 350000

65					70					75				80	
Asn	Lys	Thr	Tyr	Asn	Ser	Asn	Leu	Phe	Phe	Trp	Phe	Phe	Pro	Ala	Gln
				85					90					95	
Ile	Gln	Pro	Glu	Asp	Ala	Pro	Val	Val	Leu	Trp	Leu	Gln	Gly	Gly	Pro
			100					105					110		
Gly	Gly	Ser	Ser	Met	Phe	Gly	Leu	Phe	Val	Glu	His	Gly	Pro	Tyr	Val
		115					120					125			
Val	Thr	Ser	Asn	Met	Thr	Leu	Arg	Asp	Arg	Asp	Phe	Pro	Trp	Thr	Thr
	130					135					140				
Thr	Leu	Ser	Met	Leu	Tyr	Ile	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser
145					150					155					160
Phe	Thr	Asp	Asp	Thr	His	Gly	Tyr	Ala	Val	Asn	Glu	Asp	Asp	Val	Ala
				165					170					175	
Arg	Asp	Leu	Tyr	Ser	Ala	Leu	Ile	Gln	Phe	Phe	Gln	Ile	Phe	Pro	Glu
			180					185					190		
Tyr	Lys	Asn	Asn	Asp	Phe	Tyr	Val	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Lys
		195					200					205			
Tyr	Val	Pro	Ala	Ile	Ala	His	Leu	Ile	His	Ser	Leu	Asn	Pro	Val	Arg
	210					215					220				
Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Gly	Tyr	Ser
225					230					235					240
Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu	Tyr	Gln	Ile
				245					250					255	
Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys	Gln	Cys	His
			260					265					270		
Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu	Ala	Phe	Glu
		275					280					285			
Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp	Pro	Ser	Tyr
	290					295					300				
Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe	Leu	Arg	Cys
305					310					315					320
Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu	Ser	Leu	Pro
				325					330					335	
Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe	Asn	Asp	Gly
			340					345					350		

for 20-554055

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
 370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
 385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
 405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His  
 435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
 450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
 465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 165

ttccatgccca cctaagggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 166

tggatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 167

agctctcaga ggctgggtcat aggg

24

&lt;210&gt; 168

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 168

gtcgggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac

50

&lt;210&gt; 169

&lt;211&gt; 2477

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 169

```

cgagggtctt tccgggtccg gaatggcaca tgtgggaatc ccagtcttgt tggctacaac 60
atctttccct ttcttaacaa gttctaacag ctgttctaac agctagtgat caggggttct 120
tcttgctgga gaagaaaggg ctgagggcag agcagggcac tctcactcag ggtgaccagc 180
tccttgccctc tctgtggata acagagcatg agaaagtga gagatgcagc ggagtggagt 240
gatggaagtc taaaatagga aggaatcttg tgtgcaatat cagactctgg gagcagttga 300
cctggagagc ctgggggagg gctgcctaa caagctttca aaaaacagga ggcacttcca 360
ctgggctggg ataagacgtg ccggtaggat aggggaagact gggtttagtc ctaatatcaa 420
attgactggc tgggtgaact tcaacagcct tttaacctct ctgggagatg aaaacgatgg 480
cttaaggggc cagaaataga gatgctttgt aaaataaaat tttaaaaaaa gcaagtattt 540
tatagcataa aggctagaga ccaaaataga taacaggatt ccctgaacat tcctaagagg 600
gagaaagtat gttaaaaata gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660
accaggatgg ggaccctggg tcaggccagc ctctttgctc ctcccgaaa ttatttttgg 720
tctgaccact ctgccttggt ttttgagaa tcatgtgagg gccaacgggg gaaggtggag 780
cagatgagca cacacaggag ccgtctctc accgcgcgcc ctctcagcat ggaacagagg 840
cagccctggc cccgggccct ggaggtggac agccgctctg tggctctgct ctcagtggtc 900
tgggtgctgc tggccccccc agcagccggc atgcctcagt tcagcacctt ccactctgag 960
aatcgtgact ggaccttcaa ccacttgacc gtccaccaag ggacgggggc cgtctatgtg 1020
ggggccatca accgggtcta taagctgaca ggcaacctga ccattccagg ggtcataag 1080
acagggccag aagaggacaa caagtctcgt taccgcgcc tcactcgtgca gcctgcagc 1140
gaagtgtca ccctcaccaa caatgtcaac aagctgctca tcattgacta ctctgagaac 1200
cgctgtctgg cctgtgggag cctctaccag ggggtctgca agctgtgctg gctggatgac 1260
ctcttcaccc tgggtggagcc atcccacaag aaggagcact acctgtccag tgtcaacaag 1320
acgggcacca tgtacggggg gattgtgcgc tctgaggggt aggatggcaa gctcttcac 1380
ggcacggctg tggatgggaa gcaggattac tccccagccc tgtccagccg gaagctgccc 1440
cgagaccctg agtctctcag catgctcgac tatgagctac acagcgattt tgtctcctct 1500
ctcatcaaga tcccttcaga caccctggcc ctgggtctcc actttgacat cttctacatc 1560
tacggctttg ctagtggggg ctttgtctac tttctcactg tccagcccca gaccctgag 1620
gggtgtggcca tcaactccgc tggagacctc ttctacacct caccgcatcg ggggtctgct 1680

```

```
<210> 170
<211> 552
<212> PRT
<213> Homo sapiens
```

```

<400> 170
Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
  1              5              10              15
Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
      20              25              30
Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
      35              40              45
Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
      50              55              60
Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
  65              70              75              80
Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
      85              90              95
Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
      100              105              110
Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
      115              120              125
Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
      130              135              140
Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
  145              150              155              160
eu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
      165              170              175

```

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys  
180 185 190

Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys  
195 200 205

Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly  
210 215 220

Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr  
225 230 235 240

Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys  
245 250 255

Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His  
260 265 270

Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala  
275 280 285

Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly  
290 295 300

Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val  
305 310 315 320

Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg  
325 330 335

Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
340 345 350

Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
355 360 365

Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
370 375 380

Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
385 390 395 400

His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
405 410 415

Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
420 425 430

Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
435 440 445

Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

450                      455                      460  
 Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr  
 465                      470                      475                      480  
 Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly  
                     485                      490                      495  
 Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val  
                     500                      505                      510  
 Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys  
                     515                      520                      525  
 Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln  
                     530                      535                      540  
 Leu Tyr Phe Leu Gly Glu Gln Arg  
 545                      550

<210> 171

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 171

tggaataaccg cctcctgcag

20

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 172

cttctgccct ttggagaaga tggc

24

<210> 173

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

100-20-55670650



<400> 173  
ggactcactg gcccaggcct tcaatatcac cagccaggac gat

42

<210> 174  
<211> 3106  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1683)  
<223> a, t, c or g

<400> 174  
aggctcccgc gcgcggctga gtgcggactg gaggtggaac ccgggtcccc gcgcttagag 60  
aacacgcgat gaccacgtgg agcctccggc ggaggccggc ccgcacgctg ggactcctgc 120  
tgctggctcgt cttgggcttc ctgggtgctc gcaggctgga ctggagcacc ctgggtccctc 180  
tgccggctccg ccatcgacag ctggggctgc aggccaaagg ctggaacttc atgctggagg 240  
attccacctt ctggatcttc gggggctcca tccactattt ccgtgtgccc agggagtact 300  
ggagggaccg cctgctgaag atgaaggcct gtggcttgaa caccctcacc acctatgttc 360  
cgtggaacct gcatgagcca gaaagaggca aatttgactt ctctgggaac ctggacctgg 420  
aggccttcgt cctgatggcc gcagagatcg ggctgtgggt gattctgcgt ccaggccccct 480  
acatctgcag tgagatggac ctccggggct tgcccagctg gctactccaa gacctggca 540  
tgaggctgag gacaacttac aagggttca ccgaagcagt ggacctttat tttgaccacc 600  
tgatgtccag ggtggtgcc ctccagtaca agcgtggggg acctatcatt gccgtgcagg 660  
tgagagaatga atatggttcc tataataaag accccgcata catgccctac gtcaagaagg 720  
cactggagga ccgtggcatt gtggaactgc tctgacttcc agacaacaag gatgggctga 780  
gcaaggggat tgtccaggga gtcttgacca ccatcaactt gcagtcaaca cagagctgc 840  
agctactgac cacccttctc ttcaacgtcc aggggactca gcccagatg gtgatggagt 900  
actggacggg gtggtttgac tcgtggggag gccctcaca tatcttggat tcttctgagg 960  
ttttgaaaac cgtgtctgcc attgtggacg ccggtcctc catcaacctc tacatgttcc 1020  
acggaggcac caactttggc ttcatgaatg gagccatgca ctccatgac tacaagtcag 1080  
atgtcaccag ctatgactat gatgctgtg tgacagaagc cggcgattac acggccaagt 1140  
acatgaagct tcgagacttc ttccggctcca tctcaggcat cctctcctc cccccacctg 1200  
accttcttcc caagatgccg tatgagccct taacgccagt cttgtacctg tctctgtggg 1260  
acgccctcaa gtacctgggg gagccaatca agtctgaaaa gcccatcaac atggagaacc 1320  
tgccagtcaa tgggggaaat ggacagtcc tgggtacat tctctatgag accagcatca 1380  
cctcgtctgg catcctcagt ggccacgtgc atgatcgggg gcagggtgtt gtgaacacag 1440  
tatccatagg attcttggac tacaagacaa cgaagattgc tgtccccctg atccagggtt 1500  
acaccgtgct gaggatcttg gtggagaatc gtgggcgagt caactatggg gagaatattg 1560  
atgaccagcg caaaggctta attggaaatc tctatctgaa tgattcacc ctgaaaaact 1620  
tcagaatcta tagcctggat atgaagaaga gcttctttca gaggttcggc ctggacaaat 1680  
gngtccct cccagaaaca cccacattac ctgctttctt cttgggtagc ttgtccatca 1740  
gtccacgcc ttgtgacacc tttctgaagc tggagggtc ggagaagggg gttgtattca 1800  
tcaatggcca gaaccttga cgttactgga acattggacc ccagaagacg ctttacctcc 1860  
caggtccctg gttgagcagc ggaatcaacc aggtcatcgt ttttgaggag acgatggcgg 1920  
gccctgcatt acagttcacg gaaaccccc acctgggcag gaaccagtac attaatgtag 1980  
cggtggcaac cctcctgct ggtgccagt ggagactgcc gcctcctct gacctgaagc 2040  
ctggtggtc ctgccccacc cctcactgca aaagcatct ctttaagtag aacctcaggg 2100  
actgggggct acagtctgcc cctgtctcag ctcaaaaccc taagcctgca gggaaaggtg 2160  
ggatggctct gggcctggct ttgttgatga tggctttcct acagccctgc tcttgtgccg 2220  
aggctgtcgg gctgtctcta ggggtgggag agctaatac atcgcccagc ctttggccct 2280

For 20' 956066

```
<210> 175
<211> 636
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> MOD_RES  
<222> (539)  
<223> Any amino acid
```

Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu  
1 5 10 15

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp  
20 25 30

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln  
35 40 45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe  
50 55 60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp  
65 70 75 80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr  
85 90 95

Val	Pro	Trp	Asn	Leu	His	Glu	Pro	Glu	Arg	Gly	Lys	Phe	Asp	Phe	Ser
			100					105					110		

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly  
115 120 125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp  
130 135 140

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu	145	150	155	160
Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp		165	170	175
His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro		180	185	190
Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp		195	200	205
Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile	210		215	220
Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly	225		230	235
Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu		245	250	255
Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro		260	265	270
Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly	275		280	285
Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala	290		295	300
Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly	305		310	315
Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys		325	330	335
Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly		340	345	350
Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile		355	360	365
Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro	370		375	380
Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu	385		390	395
Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu		405	410	415
Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu		420	425	430

```
<400> 176
ggggacgcgg agctgagagg ctccgggcta gctaggtgta ggggtggacg ggtcccagga 60
ccctggtgag ggttctctac ttggccttcg gtgggggtca agacgcaggc acctacgcca 120
aaggggagca aagccgggct cggccccagg ccccaggac ctccatctcc caatgttgga 180
ggaatccgac acgtgacggt ctgtccgcgc tctcagacta gaggagcgct gtaaacgcca 240
tggtcccaa gaagctgtcc tgccttcggt ccctgctgct gccgctcagc ctgacgctac 300
tgctgcccc a ggcagacact cggtcgttcg tagtggatag gggtcatgac cggtttctcc 360
tagacggggc cccgttccgc tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420
```

tgctttgggc cgaccggctt ttgaagatgc gatggagcgg cctcaacgcc atacagtttt 480  
 atgtgccctg gaactaccac gagccacagc ctgggggtcta taactttaat ggcagccggg 540  
 acctcattgc ctttctgaat gaggcagctc tagcgaacct gttggtcata ctgagaccag 600  
 gaccttacat ctgtgcagag tgggagatgg ggggtctccc atcctggttg cttcgaaaac 660  
 ctgaaattca tctaagaacc tcagatccag acttccttgc cgcagtggac tcctggttca 720  
 aggtcttgct gcccagata tatccatggc tttatcacia tgggggcaac atcattagca 780  
 ttcaggtgga gaatgaatat ggtagctaca gagcctgtga cttcagctac atgaggcact 840  
 tggctgggct cttccgtgca ctgctaggag aaaagatctt gctcttcacc acagatgggc 900  
 ctgaaggact caagtgtggc tccctccggg gactctatac cactgtagat tttggcccag 960  
 ctgacaacat gaccaaatac tttaccctgc ttcggaagta tgaacccat gggccattgg 1020  
 taaactctga gtactacaca ggctggctgg attactgggg ccagaatcac tccacacggg 1080  
 ctgtgtcagc tgtaaccaaa ggactagaga acatgctcaa gttgggagcc agtgtgaaca 1140  
 tgtacatgtt ccattggagg accaactttg gatattggaa tgggtccgat aagaaggagc 1200  
 gcttccttcc gattactacc agctatgact atgatgcacc tatactctgaa gcaggggacc 1260  
 ccacacctaa gctttttgct cttcgagatg tcatcagcaa gttccaggaa gttcctttgg 1320  
 gacctttacc tcccccgagc cccaagatga tgcttgacc tgtgactctg cacctgggtg 1380  
 ggcatttact ggcttttcta gacttgctt gccccgtgg gccattcat tcaatcttgc 1440  
 caatgacctt tgaggctgtc aagcaggacc atggcttcat gttgtaccga acctatatga 1500  
 cccataccat ttttgagcca acaccattct ggggtccaaa taatggagtc catgaccgtg 1560  
 cctatgtgat ggtggatggg gtgttccagg gtgttgtgga gcgaaatatg agagacaaaac 1620  
 tatttttgac ggggaaactg ggggtccaaac tggatatctt ggtggagaac atggggaggc 1680  
 tcagctttgg gtctaacagc agtgacttca agggcctgtt gaagccacca attctggggc 1740  
 aaacaatcct taccagtggt atgatgttcc ctctgaaaat tgataacctt gtgaagtggg 1800  
 ggtttccctt ccagttgcc aatggccat atcctcaagc tcttcttggc cccacattct 1860  
 actccaaaac atttccaatt ttaggctcag ttggggacac atttctatat ctacctggat 1920  
 ggaccaaggg ccaagtctgg atcaatgggt ttaacttggg ccggtactgg acaaagcagg 1980  
 ggccacaaca gacctctac gtgccaagat tctgtctgtt tcttagggga gccctcaaca 2040  
 aaattacatt gctggaacta gaagatgtac ctctccagcc ccaagtccaa tttttggata 2100  
 agcctatcct caatagcact agtactttgc acaggacaca tatcaattcc ctttcagctg 2160  
 atacactgag tgctctgtaa ccaatggagt taagtgggca ctgaaaggta ggccgggcat 2220  
 ggtggctcat gcctgtaac ccagcacttt gggaggctga gacgggtgga ttacctgagg 2280  
 tcaggacttc aagaccagcc tggccaacat ggtgaaaccc cgtctccact aaaaatacaa 2340  
 aaattagccg ggcgtgatgg tgggcacctc taatcccagc tacttgggag gctgagggca 2400  
 ggagaattgc ttgaatccag gaggcagagg ttgcagttag tggagggtgt accactgcac 2460  
 tccagcctgg ctgacagtga gacactccat ctcaaaaaaa aaaaa 2505

<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu  
 1 5 10 15

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val  
 20 25 30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr  
 35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala  
 50 55 60

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe  
 65 70 75 80  
 Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe  
 85 90 95  
 Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala  
 100 105 110  
 Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp  
 115 120 125  
 Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His  
 130 135 140  
 Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe  
 145 150 155 160  
 Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly  
 165 170 175  
 Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala  
 180 185 190  
 Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu  
 195 200 205  
 Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu  
 210 215 220  
 Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro  
 225 230 235 240  
 Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro  
 245 250 255  
 His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr  
 260 265 270  
 Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly  
 275 280 285  
 Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe  
 290 295 300  
 His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly  
 305 310 315 320  
 Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser  
 325 330 335  
 Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

340	345	350
Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro		
355	360	365
Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu		
370	375	380
Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu		
385	390	395
		400
Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr		
	405	410
		415
Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val		
	420	425
		430
Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val		
435	440	445
Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr		
450	455	460
Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg		
465	470	475
		480
Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro		
	485	490
		495
Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu		
500	505	510
Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys		
515	520	525
Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr		
530	535	540
Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly		
545	550	555
		560
Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr		
565	570	575
Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu		
580	585	590
Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu		
595	600	605
Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu		
610	615	620

FOR 900000

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala  
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His  
 645 650

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 178

tggctactcc aagaccctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 179

tggacaaatc cccttgctca gccc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 180

gggcttcacc gaagcagtgg acctttatatt tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 181

ccagctatga ctatgatgca cc

22



<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

```
<210> 183
<211> 50
<212> DNA
<213> Artificial Sequence
```

```
<210> 184
<211> 1947
<212> DNA
<213> Homo sapiens
```

<400> 184						
gctttgaaca	cgtctgcaag	cccaaagtgtg	agcatctgat	tggttatgag	gtattttgagt	60
gcacccacaa	tatggcttac	atgttgaaaa	agcttctcat	cagttacata	tccattatttt	120
gtgtttatgg	ctttatctgc	ctctacactc	tcttctgggt	attcaggata	cctttgaagg	180
aatattcttt	cgaaaaagtc	agagaagaga	gcagtttttag	tgacattcca	gatgtcaaaa	240
acgattttgc	gttccttctt	cacatggtag	accagtatga	ccagctatat	tccaagcggt	300
ttgggtgtgt	cttgtcagaa	gttagtgaaa	ataaaacttag	ggaaattagt	ttgaaccatg	360
agtggacatt	tgaaaaactc	aggcagcaca	tttcacgcaa	cgcccaggac	aagcaggagt	420
tgcatctggt	catgctgtcg	ggggtgcccg	atgctgtctt	tgacctcaca	gacctggatg	480
tgctaaagct	tgaactaatt	ccagaagcta	aaattcctgc	taagatttct	caaatgacta	540
acctccaaga	gctccacctc	tgccactgcc	ctgcaaaaagt	tgaacagact	gcttttagct	600
ttcttcgcga	tcacttgaga	tgcttccacg	tgaagttcac	tgatgtggct	gaaattcctg	660
ccctgggtgta	tttgctcaaa	aaccttcgag	agttgtactt	aataggcaat	ttgaactctg	720
aaaacaataa	gatgatagga	cttgaatctc	tccgagagtt	gcggcacctt	aagatttctcc	780
acgtgaagag	caatttgacc	aaagttccct	ccaacattac	agatgtggct	ccacatctta	840
caaagttagt	cattcataat	gacggcacta	aactcttggt	actgaacagc	cttaagaaaa	900
tgatgaatgt	cgctgagctg	gaactccaga	actgtgagct	agagagaatc	ccacatgcta	960
ttttcagcct	ctctaattta	caggaaactgg	atttaaagtc	caataacatt	cgcacaattg	1020
aggaaatcat	cagtttccag	cattttaaacc	gactgacttg	tttaaaatta	tggcataaca	1080
aaattgttac	tattcctccc	tctattaccc	atgtcaaaaa	cttgggagtc	ctttatttct	1140
ctaacaacaa	gctcgaatcc	ttaccagtg	cagtatttag	tttacagaaa	ctcagatgct	1200
tagatgtgag	ctacaacaac	atttcaatga	ttccaataga	aataggattg	cttcagaacc	1260
tgcagcattt	gcatatcact	gggaacaaa	tggaacattct	gccaaaacaa	ttgtttaaat	1320



Ala	Glu	Ile	Pro	Ala	Trp	Val	Tyr	Leu	Leu	Lys	Asn	Leu	Arg	Glu	Leu	
	195						200					205				
Tyr	Leu	Ile	Gly	Asn	Leu	Asn	Ser	Glu	Asn	Asn	Lys	Met	Ile	Gly	Leu	
	210					215					220					
Glu	Ser	Leu	Arg	Glu	Leu	Arg	His	Leu	Lys	Ile	Leu	His	Val	Lys	Ser	
225					230					235					240	
Asn	Leu	Thr	Lys	Val	Pro	Ser	Asn	Ile	Thr	Asp	Val	Ala	Pro	His	Leu	
				245					250					255		
Thr	Lys	Leu	Val	Ile	His	Asn	Asp	Gly	Thr	Lys	Leu	Leu	Val	Leu	Asn	
			260					265					270			
Ser	Leu	Lys	Lys	Met	Met	Asn	Val	Ala	Glu	Leu	Glu	Leu	Gln	Asn	Cys	
		275					280					285				
Glu	Leu	Glu	Arg	Ile	Pro	His	Ala	Ile	Phe	Ser	Leu	Ser	Asn	Leu	Gln	
	290					295					300					
Glu	Leu	Asp	Leu	Lys	Ser	Asn	Asn	Ile	Arg	Thr	Ile	Glu	Glu	Ile	Ile	
305					310					315					320	
Ser	Phe	Gln	His	Leu	Lys	Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	His	Asn	
				325					330					335		
Lys	Ile	Val	Thr	Ile	Pro	Pro	Ser	Ile	Thr	His	Val	Lys	Asn	Leu	Glu	
			340					345					350			
Ser	Leu	Tyr	Phe	Ser	Asn	Asn	Lys	Leu	Glu	Ser	Leu	Pro	Val	Ala	Val	
	355						360					365				
Phe	Ser	Leu	Gln	Lys	Leu	Arg	Cys	Leu	Asp	Val	Ser	Tyr	Asn	Asn	Ile	
	370					375					380					
Ser	Met	Ile	Pro	Ile	Glu	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	His	Leu	
385					390					395					400	
His	Ile	Thr	Gly	Asn	Lys	Val	Asp	Ile	Leu	Pro	Lys	Gln	Leu	Phe	Lys	
			405						410					415		
Cys	Ile	Lys	Leu	Arg	Thr	Leu	Asn	Leu	Gly	Gln	Asn	Cys	Ile	Thr	Ser	
			420					425					430			
Leu	Pro	Glu	Lys	Val	Gly	Gln	Leu	Ser	Gln	Leu	Thr	Gln	Leu	Glu	Leu	
	435					440						445				
Lys	Gly	Asn	Cys	Leu	Asp	Arg	Leu	Pro	Ala	Gln	Leu	Gly	Gln	Cys	Arg	
	450					455					460					
Met	Leu	Lys	Lys	Ser	Gly	Leu	Val	Val	Glu	Asp	His	Leu	Phe	Asp	Thr	

465                                      470                                      475                                      480

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro

                                    485                                      490                                      495

Phe Ala Asn Gly Ile

                                    500

<210> 186  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 186  
 cctccctcta ttacccatgt c 21

<210> 187  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 187  
 gaccaacttt ctctgggagt gagg 24

<210> 188  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 188  
 gtcactttat ttctctaaca acaagctcga atccttacca gtggcag 47

<210> 189  
 <211> 2917  
 <212> DNA  
 <213> Homo sapiens

<400> 189  
 cccacgcgtc cggccttctc tctggacttt gcatttccat tccttttcat tgacaaactg 60  
 acttttttta tttctttttt tocatctctg ggccagcttg ggatcctagg ccgccttggg 120  
 aagacatttg tgttttacac acataaggat ctgtgttttg gggtttcttct tcctcccttg 180

acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240  
gcacttatct gcttaggtac atcgaagtct tttgacctcc atacagtgat tatgacctgtc 300  
atcgctgggtg gtatcctggc ggccttgctc ctgctgatag ttgtcgtgct ctgtctttac 360  
ttcaaaatac acaacgcgt aaaagctgca aaggaacctg aagctgtggc tgtaaaaaat 420  
cacaaccag acaaggtgtg gtgggccaag aacagccagg ccaaaacat tgccacggag 480  
tcttgctctg cctgacgtg ctgtgaagga tatagaatgt gtgccagttt tgattccctg 540  
ccaccttgct gttgcgacat aaatgagggc ctctgagtta ggaaaggctc ccttctcaaa 600  
gcagagccct gaagacttca atgatgtcaa tgaggccacc tgtttgtgat gtgcaggcac 660  
agaagaaaagg cacagctccc catcagtttc atggaaaata actcagtgcc tgctgggaac 720  
cagctgctgg agatccctac agagagcttc cactgggggc aaccttcca ggaaggagt 780  
ggggagagag aacctcact gtggggaatg ctgataaacc agtcacacag ctgctctatt 840  
ctcacacaaa tctacctctt gcgtggctgg aactgacgtt tcctggagg tgtccagaaa 900  
gctgatgtaa cacagagcct ataaaagctg tcggctctta aggctgcca gcgccttgcc 960  
aaaatggagc ttgtaagaag gctcatgcca ttgacctct taattctctc ctgtttggcg 1020  
gagctgacaa tggcggaggc tgaaggcaat gcaagctgca cagtcagtct agggggtgcc 1080  
aatatggcag agaccacaa agccatgatc ctgcaactca atcccagtga gaactgcacc 1140  
tggacaatag aaagaccaga aaacaaaagc atcagaatta tcttttcta tgtccagctt 1200  
gatccagatg gaagctgtga aagtgaaac attaaagtct ttgacggaac ctccagcaat 1260  
gggcctctgc tagggcaagt ctgcagtaaa aacgactatg ttccctgtatt tgaatcatca 1320  
tccagtacat tgacgtttca aatagttact gactcagcaa gaattcaaag aactgtcttt 1380  
gtcttctact acttctctc tctaacatc tctattccaa actgtggcgg ttacctggat 1440  
accttgaag gatccttcac cagcccaat taccaaaagc cgcacctga gctggcttat 1500  
tgtgtgtggc acatacaagt ggagaaagat tacaagataa aactaaactt caaagagatt 1560  
ttctagaaa tagacaaaca gtgcaaattt gattttcttg ccatctatga tggccctctc 1620  
accaactctg gctgattgg acaagtctgt ggccgtgtga ctcccactt cgaatcgta 1680  
tcaaactctc tgactgtcgt gttgtctaca gattatgcca attcttaccg gggattttct 1740  
gcttcctaca cctcaattta tgcagaaaac atcaacacta catotttaac ttgctcttct 1800  
gacaggatga gagttattat aagcaaatcc tacctagagg cttttaactc taatgggaat 1860  
aacttgcaac taaaagacct aacttgca ccaaaattat caaatgttgt ggaattttct 1920  
gtccctctta atggatgtgg tacaatcaga aaggtagaag atcagtcaat tacttacacc 1980  
aatataatca ccttttctgc atcctcaact tctgaagtga tcaccctgta gaaacaactc 2040  
cagattattg tgaagtgtga aatgggacat aattctacag tggagataat atacataaca 2100  
gaagatgatg taatacaaag tcaaaatgca ctgggcaaat ataacaccag catggctctt 2160  
tttgaatcca attcatttga aaagactata cttgaatcac catattatgt ggatttgaac 2220  
caaactcttt ttgttcaagt tagtctgcac acctcagatc caaatttggt ggtgtttctt 2280  
gatacctgta gagcctctcc cacctctgac tttgcactc caacctacga cctaatcaag 2340  
agtggatgta gtcgagatga aacttgtaag gtgtatccct tatttggaca ctatgggaga 2400  
ttccagttta atgcctttaa attcttgaga agtatgagct ctgtgtatct gcagtgtaaa 2460  
gttttgatat gtgatagcag tgaccaccag tctcgtgca atcaaggttg tgtctccaga 2520  
agcaaacgag acatttcttc atataaatgg aaaacagatt ccatcatagg acccattcgt 2580  
ctgaaaaggg atcgaagtgc aagtggcaat tcaggatttc agcatgaaac acatgcggaa 2640  
gaaactccaa accagccttt caacagtgtg catctgtttt cttcatggt tctagctctg 2700  
aatgtggtga ctgtagcgac aatcacagtg aggcattttg taaatcaacg ggcagactac 2760  
aaataccaga agctgcagaa ctattaacta acaggtccaa ccctaagtga gacatgtttc 2820  
tccaggatgc caaaggaaat gctacctcgt ggctacacat attatgaata aatgaggaag 2880  
ggcctgaaag tgacacacag gctgcatgt aaaaaaa 2917

&lt;210&gt; 190

&lt;211&gt; 607

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 190

Met	Glu	Leu	Val	Arg	Arg	Leu	Met	Pro	Leu	Thr	Leu	Leu	Ile	Leu	Ser	
1				5					10					15		
Cys	Leu	Ala	Glu	Leu	Thr	Met	Ala	Glu	Ala	Glu	Gly	Asn	Ala	Ser	Cys	
		20						25					30			
Thr	Val	Ser	Leu	Gly	Gly	Ala	Asn	Met	Ala	Glu	Thr	His	Lys	Ala	Met	
		35					40					45				
Ile	Leu	Gln	Leu	Asn	Pro	Ser	Glu	Asn	Cys	Thr	Trp	Thr	Ile	Glu	Arg	
	50					55					60					
Pro	Glu	Asn	Lys	Ser	Ile	Arg	Ile	Ile	Phe	Ser	Tyr	Val	Gln	Leu	Asp	
	65				70					75					80	
Pro	Asp	Gly	Ser	Cys	Glu	Ser	Glu	Asn	Ile	Lys	Val	Phe	Asp	Gly	Thr	
				85					90					95		
Ser	Ser	Asn	Gly	Pro	Leu	Leu	Gly	Gln	Val	Cys	Ser	Lys	Asn	Asp	Tyr	
		100						105					110			
Val	Pro	Val	Phe	Glu	Ser	Ser	Ser	Ser	Thr	Leu	Thr	Phe	Gln	Ile	Val	
		115					120					125				
Thr	Asp	Ser	Ala	Arg	Ile	Gln	Arg	Thr	Val	Phe	Val	Phe	Tyr	Tyr	Phe	
	130					135					140					
Phe	Ser	Pro	Asn	Ile	Ser	Ile	Pro	Asn	Cys	Gly	Gly	Tyr	Leu	Asp	Thr	
	145				150					155					160	
Leu	Glu	Gly	Ser	Phe	Thr	Ser	Pro	Asn	Tyr	Pro	Lys	Pro	His	Pro	Glu	
				165					170					175		
Leu	Ala	Tyr	Cys	Val	Trp	His	Ile	Gln	Val	Glu	Lys	Asp	Tyr	Lys	Ile	
			180					185					190			
Lys	Leu	Asn	Phe	Lys	Glu	Ile	Phe	Leu	Glu	Ile	Asp	Lys	Gln	Cys	Lys	
	195						200					205				
Phe	Asp	Phe	Leu	Ala	Ile	Tyr	Asp	Gly	Pro	Ser	Thr	Asn	Ser	Gly	Leu	
	210					215					220					
Ile	Gly	Gln	Val	Cys	Gly	Arg	Val	Thr	Pro	Thr	Phe	Glu	Ser	Ser	Ser	
	225				230					235					240	
Asn	Ser	Leu	Thr	Val	Val	Leu	Ser	Thr	Asp	Tyr	Ala	Asn	Ser	Tyr	Arg	
				245					250					255		
Gly	Phe	Ser	Ala	Ser	Tyr	Thr	Ser	Ile	Tyr	Ala	Glu	Asn	Ile	Asn	Thr	
			260					265					270			
Thr	Ser	Leu	Thr	Cys	Ser	Ser	Asp	Arg	Met	Arg	Val	Ile	Ile	Ser	Lys	
		275					280					285				

Ser	Tyr	Leu	Glu	Ala	Phe	Asn	Ser	Asn	Gly	Asn	Asn	Leu	Gln	Leu	Lys
290						295					300				
Asp	Pro	Thr	Cys	Arg	Pro	Lys	Leu	Ser	Asn	Val	Val	Glu	Phe	Ser	Val
305					310					315					320
Pro	Leu	Asn	Gly	Cys	Gly	Thr	Ile	Arg	Lys	Val	Glu	Asp	Gln	Ser	Ile
				325					330					335	
Thr	Tyr	Thr	Asn	Ile	Ile	Thr	Phe	Ser	Ala	Ser	Ser	Thr	Ser	Glu	Val
			340					345					350		
Ile	Thr	Arg	Gln	Lys	Gln	Leu	Gln	Ile	Ile	Val	Lys	Cys	Glu	Met	Gly
		355					360					365			
His	Asn	Ser	Thr	Val	Glu	Ile	Ile	Tyr	Ile	Thr	Glu	Asp	Asp	Val	Ile
	370					375					380				
Gln	Ser	Gln	Asn	Ala	Leu	Gly	Lys	Tyr	Asn	Thr	Ser	Met	Ala	Leu	Phe
385					390					395					400
Glu	Ser	Asn	Ser	Phe	Glu	Lys	Thr	Ile	Leu	Glu	Ser	Pro	Tyr	Tyr	Val
				405					410					415	
Asp	Leu	Asn	Gln	Thr	Leu	Phe	Val	Gln	Val	Ser	Leu	His	Thr	Ser	Asp
			420					425					430		
Pro	Asn	Leu	Val	Val	Phe	Leu	Asp	Thr	Cys	Arg	Ala	Ser	Pro	Thr	Ser
		435					440					445			
Asp	Phe	Ala	Ser	Pro	Thr	Tyr	Asp	Leu	Ile	Lys	Ser	Gly	Cys	Ser	Arg
	450					455					460				
Asp	Glu	Thr	Cys	Lys	Val	Tyr	Pro	Leu	Phe	Gly	His	Tyr	Gly	Arg	Phe
465					470					475					480
Gln	Phe	Asn	Ala	Phe	Lys	Phe	Leu	Arg	Ser	Met	Ser	Ser	Val	Tyr	Leu
				485					490					495	
Gln	Cys	Lys	Val	Leu	Ile	Cys	Asp	Ser	Ser	Asp	His	Gln	Ser	Arg	Cys
			500					505					510		
Asn	Gln	Gly	Cys	Val	Ser	Arg	Ser	Lys	Arg	Asp	Ile	Ser	Ser	Tyr	Lys
		515					520					525			
Trp	Lys	Thr	Asp	Ser	Ile	Ile	Gly	Pro	Ile	Arg	Leu	Lys	Arg	Asp	Arg
	530					535					540				
Ser	Ala	Ser	Gly	Asn	Ser	Gly	Phe	Gln	His	Glu	Thr	His	Ala	Glu	Glu
545					550					555					560
Thr	Pro	Asn	Gln	Pro	Phe	Asn	Ser	Val	His	Leu	Phe	Ser	Phe	Met	Val

565 570 575  
 Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe  
 580 585 590  
 Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr  
 595 600 605  
 <210> 191  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
 <400> 191  
 tctctattcc aaactgtggc g 21  
 <210> 192  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
 <400> 192  
 tttgatgacg attcgaaggt gg 22  
 <210> 193  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
 <400> 193  
 ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc 47  
 <210> 194  
 <211> 2362  
 <212> DNA  
 <213> Homo sapiens  
 <400> 194  
 gacggaagaa cagcgctccc gaggccgcgg gagcctgcag agaggacagc cggcctgcgc 60  
 cgggacatgc ggccccagga gctccccagg ctgcgcgttcc cggtgctgct gttgctgttg 120  
 ctgctgctgc cgccgcgcgc gtgcccctgcc cacagcgcca cgcgcttcga cccacactgg 180



```
<210> 195
<211> 467
<212> PRT
<213> Homo sapiens
```

```

<400> 195
Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu
 1          5          10          15
Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr
 20          25          30
Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
 35          40          45

```

Trp	Phe	Asp	Gln	Ala	Lys	Phe	Gly	Ile	Phe	Ile	His	Trp	Gly	Val	Phe	50	55	60
Ser	Val	Pro	Ser	Phe	Gly	Ser	Glu	Trp	Phe	Trp	Trp	Tyr	Trp	Gln	Lys	65	70	80
Glu	Lys	Ile	Pro	Lys	Tyr	Val	Glu	Phe	Met	Lys	Asp	Asn	Tyr	Pro	Pro	85	90	95
Ser	Phe	Lys	Tyr	Glu	Asp	Phe	Gly	Pro	Leu	Phe	Thr	Ala	Lys	Phe	Phe	100	105	110
Asn	Ala	Asn	Gln	Trp	Ala	Asp	Ile	Phe	Gln	Ala	Ser	Gly	Ala	Lys	Tyr	115	120	125
Ile	Val	Leu	Thr	Ser	Lys	His	His	Glu	Gly	Phe	Thr	Leu	Trp	Gly	Ser	130	135	140
Glu	Tyr	Ser	Trp	Asn	Trp	Asn	Ala	Ile	Asp	Glu	Gly	Pro	Lys	Arg	Asp	145	150	155
Ile	Val	Lys	Glu	Leu	Glu	Val	Ala	Ile	Arg	Asn	Arg	Thr	Asp	Leu	Arg	165	170	175
Phe	Gly	Leu	Tyr	Tyr	Ser	Leu	Phe	Glu	Trp	Phe	His	Pro	Leu	Phe	Leu	180	185	190
Glu	Asp	Glu	Ser	Ser	Ser	Phe	His	Lys	Arg	Gln	Phe	Pro	Val	Ser	Lys	195	200	205
Thr	Leu	Pro	Glu	Leu	Tyr	Glu	Leu	Val	Asn	Asn	Tyr	Gln	Pro	Glu	Val	210	215	220
Leu	Trp	Ser	Asp	Gly	Asp	Gly	Gly	Ala	Pro	Asp	Gln	Tyr	Trp	Asn	Ser	225	230	235
Thr	Gly	Phe	Leu	Ala	Trp	Leu	Tyr	Asn	Glu	Ser	Pro	Val	Arg	Gly	Thr	245	250	255
Val	Val	Thr	Asn	Asp	Arg	Trp	Gly	Ala	Gly	Ser	Ile	Cys	Lys	His	Gly	260	265	270
Gly	Phe	Tyr	Thr	Cys	Ser	Asp	Arg	Tyr	Asn	Pro	Gly	His	Leu	Leu	Pro	275	280	285
His	Lys	Trp	Glu	Asn	Cys	Met	Thr	Ile	Asp	Lys	Leu	Ser	Trp	Gly	Tyr	290	295	300
Arg	Arg	Glu	Ala	Gly	Ile	Ser	Asp	Tyr	Leu	Thr	Ile	Glu	Glu	Leu	Val	305	310	315
Lys	Gln	Leu	Val	Glu	Thr	Val	Ser	Cys	Gly	Gly	Asn	Leu	Leu	Met	Asn	325	330	335

<210> 198

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 198  
 aacttgccgc atcagccact ctgc

24

<210> 199  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 199  
 ttccgtgccc agcttcggta gcgagtgggt ctggtggtat tggca

45

<210> 200  
 <211> 2372  
 <212> DNA  
 <213> Homo sapiens

<400> 200  
 agcagggaaa tccggatgtc tccggttatga agtggagcag tgagtgtgag cctcaacata 60  
 gttccagaac tctccatccg gactagttat tgagcatctg cctctcatat caccagtggc 120  
 catctgaggt gtttcccttg ctctgaagggt gtaggcacga tggccagggtg cttcagcctg 180  
 gtgttgcttc tcacttccat ctggaccacg aggtccttg tccaaggctc tttgcgtgca 240  
 gaagagcttt ccatccaggt gtcattgcaga attatgggga tcacccttgt gagcaaaaag 300  
 gcgaaccagc agctgaattt cacagaagct aaggaggcct gtaggctgct gggactaagt 360  
 ttggccggca aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420  
 ggctgggttg gagatggatt cgtgggtcatc tctaggatta gcccacaccc caagtgtggg 480  
 aaaaatgggg tgggtgtcct gatttggag gttccagtga gccgacagtt tgcagcctat 540  
 tgttacaact catctgatac ttggactaac tcgtgcattc cagaaattat caccacaaa 600  
 gatcccatat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgcagct 660  
 acctactcgg tggcatcccc ttactctaca atacctgccc ctactactac tctcctgct 720  
 ccagcttcca cttctattcc acggagaaaa aaattgattt gtgtcacaga agtttttatg 780  
 gaaactagca ccatgtctac agaaactgaa ccatttggtg aaaataaagc agcattcaag 840  
 aatgaagctg ctgggttttg aggtgtcccc acggctctgc tagtgcttgc tctcctcttc 900  
 tttggtgctg cagctggtct tggattttgc tatgtcaaaa ggtatgtgaa ggccttcctt 960  
 ttacaaaaca agaatacagca gaaggaaatg atcgaaacca aagtagtaaa ggaggagaag 1020  
 gccaatgata gcaaccctaa tgaggaatca aagaaaactg ataaaaaccc agaagagtc 1080  
 aagagtccaa gcaaaactac cgtgcgatgc ctggaagctg aagtttagat gagacagaaa 1140  
 tgaggagaca cacctgaggc tggtttcttt catgctcctt accctgcccc agctggggaa 1200  
 atcaaaaggc ccaaagaacc aaagaagaaa gttccaccct gggtcctaac tggaaatcagc 1260  
 tcaggactgc cattggacta tggagtgcac caaagagaat gcccttctcc ttattgtaac 1320  
 cctgtctgga tctatctctc ctacctccaa agcttcccac ggcttttcta ggcctgctat 1380  
 gtcttaataa tatccactg ggagaaagga gttttgcaaa gtgcaaggac ctaaaacatc 1440

104720" 95640660

tcatcagtat ccagtggtaa aaaggcctcc tggctgtctg aggctaggtg ggttgaaagc 1500  
 caaggagtca ctgagaccaa ggctttctct actgattccg cagctcagac cctttcttca 1560  
 gctctgaaag agaaacacgt atcccacctg acatgtcctt ctgagcccg taagagcaaa 1620  
 agaatggcag aaaagtttag cccctgaaag ccatggagat tctcataact tgagacctaa 1680  
 tctctgtaaa gctaaaataa agaaatagaa caaggctgag gatacgacag tacactgtca 1740  
 gcagggactg taaacacaga cagggtcaaa gtgttttctc tgaacacatt gagttggaat 1800  
 cactgttttag aacacacaca cttacttttt ctggctctcta ccactgctga tattttctct 1860  
 aggaaatata cttttacaag taacaaaaat aaaaactctt ataaatttct atttttatct 1920  
 gagttacaga aatgattact aaggaagatt actcagtaat ttgttttaaaa agtaataaaa 1980  
 ttcaacaaac atttgctgaa tagctactat atgtcaagtg ctgtgcaagg tattacactc 2040  
 tgtaattgaa tattattcct caaaaaattg cacatagtag aacgctatct ggggaagctat 2100  
 ttttttcagt tttgatattt ctagcttatt tacttccaaa ctaattttta tttttgtgta 2160  
 gactaatctt attcattttc tctaatatgg caaccattat aaccttaatt tattattaac 2220  
 atacctaaga agtacattgt tacctctata taccaaagca catttttaaaa gtgccattaa 2280  
 caaatgtatc actagccctc ctttttccaa caagaaggga ctgagagatg cagaaatatt 2340  
 tgtgacaaaa aattaaagca tttagaaaac tt 2372

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr  
 1 5 10 15

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile  
 20 25 30

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala  
 35 40 45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu  
 50 55 60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala  
 65 70 75 80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val  
 85 90 95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly  
 100 105 110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys  
 115 120 125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile  
 130 135 140

0904956 044

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
 145 150 155 160  
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
 165 170 175  
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
 180 185 190  
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
 210 215 220  
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
 225 230 235 240  
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
 245 250 255  
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
 260 265 270  
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
 275 280 285  
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
 290 295 300  
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala  
 305 310 315 320  
 Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 202

gagctttcca tccaggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence



&lt;222&gt; (1003)

&lt;223&gt; a, t, c or g

&lt;400&gt; 206

```

agatggcggg cttggcacct ctaattgctc tcgtgtattc ggtgcccgcga ctttcacgat 60
ggctcgccca accttactac cttctgtcgg cctgtctctc tgctgccttc ctactcgtga 120
ggaaactgcc gccgctctgc cacggctctgc ccaccaacg cgaagacggg aacccgtgtg 180
actttgactg gagagaagtg gagatcctga tgtttctcag tgccattgtg atgatgaaga 240
accgcagatc catcactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300
ccaacacaat tcttttcttc cgcttgataa ttgcgatggg cctactttac atcacactct 360
gcatagtgtt cctgatgacg tgcaaacccc ccctatatat gggccctgag tatatcaagt 420
acttcaatga taaaaccatt gatgaggaac tagaacggga caagaggggtc acttggattg 480
tggagttctt tgccaattgg tctaataact gccaatcatt tgccctctac tatgctgacc 540
tctcccttaa atacaactgt acagggctaa attttgggaa ggtggatgtt ggacgctata 600
ctgatgttag tacgcggtac aaagttagca catcacccct caccaagcaa ctccctaccc 660
tgatcctgtt ccaaggtggc aaggaggcaa tgcggcggcc acagattgac aagaaaggac 720
gggctgtctc atggaccttc tctgaggaga atgtgatccg agaatttaac ttaaataagc 780
tataccagcg ggccaagaaa ctatcaaagg ctggagacaa tatccctgag gagcagcctg 840
tggcttcaac cccaccaca gtgtcagatg gggaaaacaa gaaggataaa taagatcctc 900
actttggcag tgcttcctct cctgtcaatt ccaggtctct tccataacca caagcctgag 960
gctgcagcct ttnattnatg ttttcctttt ggctgngact ggntggggca gcatgcagct 1020
tctgatttta aagaggcatc tagggaattg tcaggcaccc tacaggaagg cctgccatgc 1080
tgtggccaac tgtttcaact gagcaagaaa gagatctcat aggacggagg gggaaatggg 1140
ttccctccaa gcttgggtca gtgtgttaac tgcttatcag ctattcagac atctccatgg 1200
tttctccatg aaactctgtg gtttcatcat tccttcttag ttgacctgca cagcttgggt 1260
agacctagat ttaaccctaa ggtaagatgc tggggtatag aacgctaaga attttcccc 1320
aaggactctt gcttccttaa gcccttctgg ctctgcttat ggtcttcatt aaaagtataa 1380
gcctaacttt gtcgctagtc ctaaggagaa acctttaacc acaaagtttt tatcattgaa 1440
gacaatattg aacaaccccc tattttgtgg ggattgagaa ggggtgaata gaggcttgag 1500
actttccttt gtgtggtagg acttggagga gaaatccct ggactttcac taaccctctg 1560
acatactccc cacaccaggt tgatggcttt ccgtaataaa aagattggga tttccttttg 1620

```

&lt;210&gt; 207

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

```

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
  1                      5                      10                      15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
          20                      25                      30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
          35                      40                      45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
          50                      55                      60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
          65                      70                      75                      80

```

F04720"SS670550



Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
                             85                            90                            95  
 Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
                             100                            105                            110  
 Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
                             115                            120                            125  
 Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys  
                             130                            135                            140  
 Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val  
   145                            150                            155                            160  
 Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile  
                             165                            170                            175  
 Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly  
                             180                            185                            190  
 Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val  
                             195                            200                            205  
 Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln  
                             210                            215                            220  
 Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg  
   225                            230                            235                            240  
 Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn  
                             245                            250                            255  
 Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp  
                             260                            265                            270  
 Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser  
                             275                            280                            285  
 Asp Gly Glu Asn Lys Lys Asp Lys  
                             290                            295

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 208

gcttgatgat tcgcatgggc ctac

<210> 209

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 209

tggagacaat atccctgagg

20

<210> 210

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 210

aacagttggc cacagcatgg cagg

24

<210> 211

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 211

ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag

50

<210> 212

<211> 1985

<212> DNA

<213> Homo sapiens

<400> 212

ggacagctcg cggcccccca gagctctagc cgtcgaggag ctgcctgggg acgtttgccc 60  
tggggcccca gcctggcccg ggtcaccctg gcatgaggag atgggcctgt tgctcctggt 120  
cccattgctc ctgctgcccg gctcctacgg actgcccttc tacaacggct tctactactc 180  
caacagcgcc aacgaccaga acctaggcaa cggatcatggc aaagacctcc ttaatggagt 240  
gaagctggtg gtggagacac ccgaggagac cctgttcacc taccaagggg ccagtgtgat 300  
cctgccctgc cgctaccgct acgagccggc cctgggtctcc ccgcggcgtg tgcgtgtcaa 360  
atggtggaag ctgtcggaga acggggcccc agagaaggac gtgctggtgg ccatcgggct 420  
gaggcaccgc tcctttgggg actaccaagg ccgcgtgcac ctgcggcagg acaaagagca 480  
tgacgtctcg ctggagatcc aggatctgcg gctggaggac tatgggcgtt accgctgtga 540  
ggtcattgac gggctggagg atgaaagcgg tctggtggag ctggagctgc ggggtgtggt 600

104720-954000

ctttccttac cagtccccca acgggagccta ccagttcaac ttccacgagg gccagcaggt 660  
 ctgtgcagag caggctgcgg tgggtggcctc ctttgagcag ctcttccggg cctgggagga 720  
 gggcctggac tggtgcaacg cgggctggct gcaggatgct acggtgcagt accccatcat 780  
 gttgccccgg cagccctgcg gtggcccagg cctggcacct ggcgtgcgaa gctacggccc 840  
 ccgccaccgc cgctgcacc gctatgatgt attctgcttc gctactgcc tcaaggggcg 900  
 ggtgtactac ctggagcacc ctgagaagct gacgctgaca gaggcaaggg aggcctgcca 960  
 ggaagatgat gccacgatcg ccaagggtgg acagctcttt gccgcctgga agttccatgg 1020  
 cctggaccgc tgcgacgctg gctggctggc agatggcagc gtccgctacc ctgtggttca 1080  
 ccgcatacct aactgtgggc cccagagcc tgggggtccga agctttggct tccccgacct 1140  
 gcagagccgc ttgtacgggtg ttactgcta ccgccagcac taggacctgg ggcctcccc 1200  
 tgcgcatttc cctcactggc tgtgtattta ttgagtgggt cgttttccct tgtgggttgg 1260  
 agccatttta actgttttta tacttctcaa tttaaatttt ctttaaacat ttttttacta 1320  
 ttttttgtaa agcaaacaga acccaatgcc tccctttgct cctggatgcc ccactccagg 1380  
 aatcatgctt gctcccctgg gccatttgcg gttttgtggg cttctggagg gttccccgcc 1440  
 atccaggctg gtctccctcc cttaaggagg ttggtgcca gagtgggagg tggcctgtct 1500  
 agaatgccgc cgggagtcgg ggcatggtgg gcacagttct ccctgcccct cagcctgggg 1560  
 gaagaagagg gcctcggggg cctccggagc tgggctttgg gcctctctg cccacctcta 1620  
 cttctctgtg aagccgctga cccagctctg cccactgagg ggctagggct ggaagccagt 1680  
 tctaggcttc caggcgaaat ctgagggag gaagaaaact ccctccccgt tccccctccc 1740  
 ctctcggttc caaagaatct gttttgtgt cathttgttc tctgtttcc ctgtgtgggg 1800  
 aggggcccctc aggtgtgtgt actttggaca ataaatggtg ctatgactgc cttccgccaa 1860  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980  
 aaaaaa 1985

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

Met Gly Leu Leu Leu Val Pro Leu Leu Leu Pro Gly Ser Tyr  
 1 5 10 15

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp  
 20 25 30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys  
 35 40 45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala  
 50 55 60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser  
 65 70 75 80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala  
 85 90 95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe  
 100 105 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

for "354060"

115                                      120                                      125  
 Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr  
     130                                      135                                      140  
 Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu  
     145                                      150                                      155                                      160  
 Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg  
                                     165                                      170                                      175  
 Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala  
                                     180                                      185                                      190  
 Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly  
                                     195                                      200                                      205  
 Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr  
     210                                      215                                      220  
 Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro  
     225                                      230                                      235                                      240  
 Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp  
                                     245                                      250                                      255  
 Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu  
                                     260                                      265                                      270  
 His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu  
                                     275                                      280                                      285  
 Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys  
     290                                      295                                      300  
 Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser  
     305                                      310                                      315                                      320  
 Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu  
                                     325                                      330                                      335  
 Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr  
                                     340                                      345                                      350  
 Gly Val Tyr Cys Tyr Arg Gln His  
     355                                      360  
 <210> 214  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
 <220>

104120" 95640650

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 215

ttcccttggtg gggtggag

18

<210> 216

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 216

agggctggaa gccagttc

18

<210> 217

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 217

agccagtgag gaaatgcg

18

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 218

tgtccaaagt acacacacct gagg

24

for seqs

```
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
```

```
<210> 220
<211> 1503
<212> DNA
<213> Homo sapiens
```

```
<210> 221
<211> 328
<212> PRT
<213> Homo sapiens
```

<400> 221  
Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Leu Arg His

1	5	10	15
Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly	20	25	30
Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala	35	40	45
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val	50	55	60
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu	65	70	75
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp	85	90	95
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg	100	105	110
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp	115	120	125
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly	130	135	140
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr	145	150	155
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp	165	170	175
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu	180	185	190
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr	195	200	205
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu	210	215	220
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala	225	230	235
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn	245	250	255
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro	260	265	270
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu	275	280	285

104720 35640660

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu  
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe



<400> 225  
 cccccctgag cgacgctccc ccatgatgac gccacggga actt

44

<210> 226  
 <211> 2403  
 <212> DNA  
 <213> Homo sapiens

<400> 226  
 ggggccttgc cttccgcact cgggcgcagc cgggtggatc tcgagcaggt gcggagcccc 60  
 gggcggcggg cgcgggtgag agggatccct gacgcctctg tccctgtttc tttgtcgctc 120  
 ccagcctgtc tgtcgctggt ttggcgcccc cgctccccg cgggtcgggg ttgcacaccg 180  
 atcctgggct tcgctcgatt tgccgcccag gcgcctccca gacctagagg ggcgctggcc 240  
 tggagcagcg ggctgctgtg gtcctctctc ctctgcgcg cgcgcgggga tccgaagggt 300  
 gcggggctct gaggaggtga cgcgcggggc ctccgcacc ctggccttgc ccgcattctc 360  
 cctctctccc aggtgtgagc agcctatcag tcaccatgtc cgcagcctgg atcccggctc 420  
 tcggcctcgg tgtgtgtctg ctgctgtctg cggggccccc gggcagcgag ggagccgctc 480  
 ccattgctat cacatgtttt accagaggct tggacatcag gaaagagaaa gcagatgtcc 540  
 tctgccagg gggctgcctt cttgaggaat tctctgtgta tgggaacata gtatatgctt 600  
 ctgtatcgag catatgtggg gctgctgtcc acaggggagt aatcagcaac tcagggggac 660  
 ctgtacgagt ctatagccta cctggctcag agatggctct cttctttcac agtaactaaa ggcaaaaagta 780  
 tccagctctca aatgctttct agatggctct cttctttcac agtaactaaa ggcaaaaagta 840  
 gtacacagga gccacagga caagcagtg ccacagcaca tccaccaaca ggtaaacgac 900  
 taaagaaaac acccgagaag aaaactggca ataaagattg taaagcagac attgcatttc 960  
 tgattgatgg aagctttaat attgggcagc gccgatttaa tttacagaag aattttgttg 1020  
 gaaaagtggc tctaattgtt ggaattggaa cagaaggacc acatgtgggc cttgttcaag 1080  
 ccagtgaaca tcccaaaaata gaattttact tgaaaaactt tacatcagcc aaagatgttt 1140  
 tgtttgccat aaaggaaagta ggtttcagag ggggtaattc caatacagga aaagccttga 1200  
 agcatactgc tcagaaattc ttcacggtag atgctggagt aagaaaaggg atcccaaaag 1260  
 tgggtgggtg atttattgat gggtggcctt ctgatgacat cgaggaagca ggcattgttg 1320  
 ccagagagtt tgggtgcaat gtatttatag tttctgtggc caagcctatc cctgaagaac 1380  
 tggggatggt tcaggatgtc acatttggtg acaaggctgt ctgtcggaat aatggcttct 1440  
 tctcttacca catgccccac tgggttggca ccacaaaata cgtaaagcct ctggtacaga 1500  
 agctgtgcac tcatgaacaa atgatgtgca gcaagacctg ttataactca gtgaacattg 1560  
 ccttttctaat tgatggctcc agcagtggtg gagatagcaa tttccgcctc atgcttgaat 1620  
 ttgtttccaa catagccaag acttttgaaa tctcggacat tggtgccaag atagctgctg 1680  
 tacagtttac ttatgatcag cgcacggagt tcagtttcac tgactatagc accaaagaga 1740  
 atgtcctagc tgtcatcaga aacatccgct atatgagtgg tggaaacagct actggtgatg 1800  
 ccatttcctt cactgttaga aatgtgtttg gccctataag ggagagcccc aacaagaact 1860  
 tcctagtaat tgtcacagat gggcagtcct atgtatgtgt ttgggtgtggc ttgggcacct ctggatgacc 1920  
 cacatgatgc aggaatcact atcttctctg ttgggtgtggc cttcacaga gagttcacag 1980  
 tgaaagatat ggcttctaaa ccgaaggagt ctcacgcttt cttcacaga gagttcacag 2040  
 gattagaacc aattgtttct gatgtcatca gaggcatttg tagagatttc ttagaatccc 2100  
 agcaataatg gtaacatttt gacaactgaa agaaaaagta caaggggagc cagtgtgtaa 2160  
 attgtattct cataatactg aaatgcttta gcatactaga atcagatata aaactattaa 2220  
 gtatgtcaac agccatttag gcaataaagc actcctttaa agccgctgcc ttctgggtac 2280  
 aatttacagt gtactttgtt aaaaacactg ctgaggcttc ataactatgg ctcttagaaa 2340  
 ctgaggaaag aggagataat gtggattaaa accttaagag ttctaaccat gcctactaaa 2400  
 tgtacagata tgcaaatcc atagctcaat aaaagaatct gatacttaga ccaaaaaaaa 2403  
 aaa

<210> 227

00445 0 144  
 104720 954066

```

<400> 227
Met Ser Ala Ala Trp Ile Pro Ala Leu Gly Leu Gly Val Cys Leu Leu
  1              5              10              15
Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile
      20              25              30
Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
      35              40              45
Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn
      50              55              60
Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg
      65              70              75              80
Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro
      85              90              95
Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln
      100             105             110
Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser
      115             120             125
Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro
      130             135             140
Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys
      145             150             155             160
Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile
      165             170             175
Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala
      180             185             190
Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln
      195             200             205
Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser
      210             215             220
Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly
      225             230             235             240
Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe
      245             250             255

```

Thr	Val	Asp	Ala	Gly	Val	Arg	Lys	Gly	Ile	Pro	Lys	Val	Val	Val	Val	
			260					265					270			
Phe	Ile	Asp	Gly	Trp	Pro	Ser	Asp	Asp	Ile	Glu	Glu	Ala	Gly	Ile	Val	
			275				280					285				
Ala	Arg	Glu	Phe	Gly	Val	Asn	Val	Phe	Ile	Val	Ser	Val	Ala	Lys	Pro	
			290				295				300					
Ile	Pro	Glu	Glu	Leu	Gly	Met	Val	Gln	Asp	Val	Thr	Phe	Val	Asp	Lys	
305					310					315						
Ala	Val	Cys	Arg	Asn	Asn	Gly	Phe	Phe	Ser	Tyr	His	Met	Pro	Asn	Trp	
				325					330					335		
Phe	Gly	Thr	Thr	Lys	Tyr	Val	Lys	Pro	Leu	Val	Gln	Lys	Leu	Cys	Thr	
			340					345					350			
His	Glu	Gln	Met	Met	Cys	Ser	Lys	Thr	Cys	Tyr	Asn	Ser	Val	Asn	Ile	
			355				360					365				
Ala	Phe	Leu	Ile	Asp	Gly	Ser	Ser	Ser	Val	Gly	Asp	Ser	Asn	Phe	Arg	
			370				375					380				
Leu	Met	Leu	Glu	Phe	Val	Ser	Asn	Ile	Ala	Lys	Thr	Phe	Glu	Ile	Ser	
385					390					395						
Asp	Ile	Gly	Ala	Lys	Ile	Ala	Ala	Val	Gln	Phe	Thr	Tyr	Asp	Gln	Arg	
				405					410					415		
Thr	Glu	Phe	Ser	Phe	Thr	Asp	Tyr	Ser	Thr	Lys	Glu	Asn	Val	Leu	Ala	
			420					425					430			
Val	Ile	Arg	Asn	Ile	Arg	Tyr	Met	Ser	Gly	Gly	Thr	Ala	Thr	Gly	Asp	
			435				440					445				
Ala	Ile	Ser	Phe	Thr	Val	Arg	Asn	Val	Phe	Gly	Pro	Ile	Arg	Glu	Ser	
			450				455					460				
Pro	Asn	Lys	Asn	Phe	Leu	Val	Ile	Val	Thr	Asp	Gly	Gln	Ser	Tyr	Asp	
465					470					475						
Asp	Val	Gln	Gly	Pro	Ala	Ala	Ala	Ala	His	Asp	Ala	Gly	Ile	Thr	Ile	
				485					490					495		
Phe	Ser	Val	Gly	Val	Ala	Trp	Ala	Pro	Leu	Asp	Asp	Leu	Lys	Asp	Met	
			500					505					510			
Ala	Ser	Lys	Pro	Lys	Glu	Ser	His	Ala	Phe	Phe	Thr	Arg	Glu	Phe	Thr	
			515				520					525				
Gly	Leu	Glu	Pro	Ile	Val	Ser	Asp	Val	Ile	Arg	Gly	Ile	Cys	Arg	Asp	
			530				535					540				

Phe Leu Glu Ser Gln Gln  
545 550

<210> 228

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 228

tggtctcgca caccgatc

18

<210> 229

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 229

ctgctgtcca caggggag

18

<210> 230

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 230

ccttgaagca tactgctc

18

<210> 231

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 231

gagatagcaa tttccgcc

18

<210> 232

104120-3367050

<211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 232  
 ttctcaaga ggcagcc

18

<210> 233  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 233  
 cttggcacca atgtccgaga ttcc

24

<210> 234  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 234  
 gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg

45

<210> 235  
 <211> 2586  
 <212> DNA  
 <213> Homo sapiens

<400> 235  
 cgccgcgctc ccgcacccgc ggcccgcgcc cgcgcgcgct cccgcatctg caccgcgagc 60  
 ccggcggcct ccggcgggga ggcagcagat ccagtccggc ccgcagcgca actcgggtcca 120  
 gtcggggcgg cggctgcggg cgcagagcgg agatgcagcg gcttggggcc accctgctgt 180  
 gcctgctgct ggcggcgggc gtccccacgg ccccgcgccc cgctccgacg ggcacctcgg 240  
 ctccagtcaa gcccgggccc gctctcagct acccgcagga ggaggccacc ctcaatgaga 300  
 tgttccgcga ggttgaggaa ctgatggagg acacgcagca caaattgcgc agcgcggtgg 360  
 aagagatgga ggcagaagaa gctgctgcta aagcatcatc agaagtgaac ctggcaaact 420  
 tacctcccag ctatcacaat gagaccaaca cagacacgaa ggttggaat aataccatcc 480  
 atgtgcaccg agaaattcac aagataacca acaaccagac tggacaaatg gtcttttcag 540  
 agacagttat cacatctgtg ggagacgaag aaggcagaag gagccacgag tgcacatcgc 600  
 acgaggactg tggggcccagc atgtactgcc agtttgccag cttccagtac acctgccagc 660  
 catgccgggg ccagaggatg ctctgcaccc gggacagtga gtgctgtgga gaccagctgt 720

104720 3564060

gtgtctgggg tcaactgcacc aaaatggcca ccaggggcag caatgggacc atctgtgaca 780  
accagaggga ctgccagccg gggctgtgct gtgccttcca gagaggcctg ctgttccctg 840  
tgtgcacacc cctgcccgtg gagggcgagc tttgccatga ccccgccagc cggcttcttg 900  
acctcatcac ctgggagcta gagcctgatg gagccttgga ccgatgccct tgtgccagt 960  
gcctcctctg ccagccccac agccacagcc tgggtgatgt gtgcaagccg accttcgtgg 1020  
ggagccgtga ccaagatggg gagatcctgc tgcccagaga ggtccccgat gagtatgaag 1080  
ttggcagctt catggaggag gtgcgccagg agctggagga cctggagagg agcctgactg 1140  
aagagatggc gctgggggag cctgcggctg ccgcccgtgc actgctggga ggggaagaga 1200  
tttagatctg gaccaggctg tgggtagatg tgcaatagaa atagctaatt tatttcccca 1260  
gggtgtgtgt ttaggcgtgg gctgaccagg cttcttctta catcttcttc ccagtaagtt 1320  
tccccctctg cttgacagca tgaggtgttg tgcatttgtt cagctcccc aggtgttct 1380  
ccaggcttca cagtctggtg cttgggagag tcaggcaggg ttaaaactgca ggagcagttt 1440  
gccacccctg tccagattat tggctgcttt gcctctacca gttggcagac agccgtttgt 1500  
tctacatggc tttgataatt gtttgagggg aggagatgga aacaatgtgg agtctccctc 1560  
tgattggttt tggggaaatg tggagaagag tgccctgctt tgcaaacatc aacctggcaa 1620  
aatgcaaca aatgaatttt ccacgcagtt ctttccatgg gcataggtaa gctgtgcctt 1680  
cagctgttgc agatgaaatg ttctgttcac cctgcattac atgtgtttat tcatccagca 1740  
gtgttgtctc gctcctacct ctgtgccagg gcagcathtt catatccaag atcaattccc 1800  
tctctcagca cagcctgggg agggggtcat tgttctctc gtccatcagg gatctcagag 1860  
gctcagagac tgcaagctgc ttgcccaagt cacacagcta gtgaagacca gagcagtttc 1920  
atctggttgt gactctaagc tcagtgtctt ctccactacc ccacaccagc cttggtgcca 1980  
ccaaaagtgc tccccaaaag gaaggagaat gggatthttc ttgaggcatg cacatctgga 2040  
attaaggtca aactaattct cacatccctc taaaagtaaa ctactgttag gaacagcagt 2100  
gttctcacag tgtggggcag ccgtccttct aatgaagaca atgatattga cactgtccct 2160  
ctttggcagt tgcattagta actttgaaag gtatatgact gagcgtagca tacaggttaa 2220  
cctgcagaaa cagtacttag gtaattgtag ggcgaggatt ataaatgaaa tttgcaaaat 2280  
cacttagcag caactgaaga caattatcaa ccacgtggag aaaatcaaac cgagcagggc 2340  
tgtgtgaaac atggttgtaa tatgcgactg cgaacactga actctacgc actccacaaa 2400  
tgatgttttc aggtgtcatg gactgttgcc accatgtatt catccagagt tcttaaagtt 2460  
taaagttgca catgattgta taagcatgct ttcttttgagt tttaaattat gtataaacat 2520  
aagttgcatt tagaaatcaa gcataaatca cttcaactgc aaaaaaaaaa aaaaaaaaaa 2580  
aaaaaa 2586

<210> 236

<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala  
1 5 10 15

Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val  
20 25 30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
35 40 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
50 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
65 70 75 80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
                             85                            90                            95  
 Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His  
                             100                            105                            110  
 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe  
                             115                            120                            125  
 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser  
                             130                            135                            140  
 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln  
                             145                            150                            155                            160  
 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met  
                             165                            170                            175  
 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp  
                             180                            185                            190  
 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys  
                             195                            200                            205  
 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
                             210                            215                            220  
 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
                             225                            230                            235                            240  
 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
                             245                            250                            255  
 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
                             260                            265                            270  
 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
                             275                            280                            285  
 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val  
                             290                            295                            300  
 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
                             305                            310                            315                            320  
 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu  
                             325                            330                            335  
 Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile  
                             340                            345                            350

&lt;210&gt; 237

<211> 17  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 237  
     ggagctgcac cccttgc 17  
  
 <210> 238  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 238  
     ggaggactgt gccaccatga gagactcttc aaacccaagg caaaattgg 49  
  
 <210> 239  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 239  
     gcagagcggg gatgcagcgg ctg 24  
  
 <210> 240  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 240  
     ttggcagctt catggagg 18  
  
 <210> 241  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 241  
     cctgggcaaa aatgcaac 18



<210> 242  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 242  
 ctccagctcc tggcgcacct cctc

24

<210> 243  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 243  
 ggctctcagc taccgcgag gagcgaggcc accctcaatg agatg

45

<210> 244  
 <211> 3679  
 <212> DNA  
 <213> Homo Sapien

<400> 244  
 aaggaggctg ggaggaaaga ggtaagaaag gttagagaac ctacctcaca 50  
 tctctctggg ctccagaagga ctctgaagat aacaataatt tcagcccatc 100  
 cactctcctt cctcccaaaa cacacatgtg catgtacaca cacacataca 150  
 cacacataca ccttctctct cttcactgaa gactcacagt cactcactct 200  
 gtgagcaggt catagaaaag gacactaaag ccttaaggac aggcttgccc 250  
 attacctctg cagctccttt ggcttggtga gtcaaaaaac atgggagggg 300  
 ccaggcacgg tgactcacac ctgtaatccc agcattttgg gagaccgagg 350  
 tgagcagatc acttgaggtc aggagttcga gaccagcctg gccaacatgg 400  
 agaaaccccc atctctacta aaaatacaaa aattagccag gagtgggtggc 450  
 aggtgcctgt aatcccagct actcaggtgg ctgagccagg agaatcgctt 500  
 gaatccagga ggcgaggat gcagtcagct gactgcaccg ctgcactcca 550  
 gcctgggtga cagaatgaga ctctgtctca aacaacaaa cacgggagga 600

TCFCA-567050

ggggtagata ctgcttctct gcaacctcct taactctgca tcctcttctt 650  
 ccagggtctgc ccttgatggg gcctggcaat gactgagcag gccagcccc 700  
 agaggacaag gaagagaagg catattgagg agggcaagaa gtgacgcccc 750  
 gtgtagaatg actgccctgg gaggggtggtt ccttggggccc tggcagggtt 800  
 gctgaccctt accctgcaaa acacaaagag caggactcca gactctcctt 850  
 gtgaatggtc ccttgccctg cagctccacc atgaggcttc tcgtggcccc 900  
 actcttgcta gcttgggtgg ctggtgccac tgccactgtg ccggtgggtac 950  
 cctggcatgt tccctgcccc cctcagtgtg cctgccagat ccggccctgg 1000  
 tatacgcccc gctcgtccta ccgcgagget accactgtgg actgcaatga 1050  
 cctattcctg acggcagtcc ccccggcact ccccgcaggc acacagacct 1100  
 tgctcctgca gagcaacagc attgtccgtg tggaccagag tgagctgggc 1150  
 tacctggcca atctcacaga gctggacctg tcccagaaca gcttttcgga 1200  
 tgcccgagac tgtgatttcc atgccctgcc ccagctgctg agcctgcacc 1250  
 tagaggagaa ccagctgacc cggctggagg accacagctt tgcagggtctg 1300  
 gccagcctac aggaactcta tctcaaccac aaccagctct accgcatcgc 1350  
 ccccagggcc ttttctggcc tcagcaactt gctgcggctg cacctcaact 1400  
 ccaacctcct gagggccatt gacagccgct ggtttgaaat gctgccaac 1450  
 ttggagatac tcatgattgg cggcaacaag gtagatgcca tcctggacat 1500  
 gaacttcggt cccctggcca acctgcgtag cctggtgcta gcaggcatga 1550  
 acctgcggga gatctccgac tatgccctgg aggggctgca aagcctggag 1600  
 agcctctcct tctatgacaa ccagctggcc cgggtgcccc ggcgggcact 1650  
 ggaacagggtg cccgggctca agttcctaga cctcaacaag aaccgctcc 1700  
 agcgggtagg gccgggggac tttgccaaca tgctgcacct taaggagctg 1750  
 ggactgaaca acatggagga gctggtctcc atcgacaagt ttgccctggt 1800  
 gaacctcccc gagctgacca agctggacat caccaataac ccacggctgt 1850  
 ccttcatcca cccccgcgc ttccaccacc tgccccagat ggagaccctc 1900  
 atgctcaaca acaacgctct cagtgccttg caccagcaga cgggtggagt 1950

000456 0740  
 101720 95640660

cctgcccaac	ctgcaggagg	taggtctcca	cggcaacccc	atccgctgtg	2000
actgtgtcat	ccgctggggc	aatgccacgg	gcacccgtgt	ccgcttcac	2050
gagccgcaat	ccaccctgtg	tgcggagcct	ccggacctcc	agcgccctcc	2100
ggtccgtgag	gtgcccttcc	gggagatgac	ggaccactgt	ttgcccctca	2150
tctccccacg	aagcttcccc	ccaagcctcc	aggtagccag	tggagagagc	2200
atggtgctgc	attgccgggc	actggccgaa	cccgaaacccg	agatctactg	2250
ggtcactcca	gctgggcttc	gactgacacc	tgcccatgca	ggcaggaggt	2300
accgggtgta	ccccgagggg	accctggagc	tgcggagggg	gacagcagaa	2350
gaggcagggc	tatacacctg	tgtggcccag	aacctgggtg	gggctgacac	2400
taagacgggt	agtgtgggtg	tgggccgtgc	tctcctccag	ccaggcaggg	2450
acgaaggaca	ggggctggag	ctccgggtgc	aggagacca	ccctatcac	2500
atcctgctat	cttgggtcac	cccacccaac	acagtgtcca	ccaacctcac	2550
ctgggtccagt	gcctcctccc	tccggggcca	ggggggccaca	gctctggccc	2600
gcctgcctcg	gggaacccac	agctacaaca	ttaccgcct	ccttcaggcc	2650
acggagtact	gggcctgcct	gcaagtggcc	tttgtgatg	cccacacca	2700
gttggcttgt	gtatggggcca	ggaccaaaga	ggccacttct	tgccacagag	2750
ccttagggga	tcgtcctggg	ctcattgcca	tcttggtct	cgctgtcctt	2800
ctcctggcag	ctgggctagc	ggccacctt	ggcacaggcc	aaccaggaa	2850
gggtgtgggt	gggaggcggc	ctctcctcc	agcctgggct	ttctggggct	2900
ggagtgcccc	ttctgtccgg	gttgtgtctg	ctcccctcgt	cctgccctgg	2950
aatccagggg	ggaagctgcc	cagatcctca	gaaggggaga	cactgttgcc	3000
accattgtct	caaaattctt	gaagctcagc	ctgttctcag	cagtagagaa	3050
atcactagga	ctacttttta	ccaaaagaga	agcagtctgg	gccagatgcc	3100
ctgccaggaa	agggacatgg	acccacgtgc	ttgaggcctg	gcagctgggc	3150
caagacagat	ggggctttgt	ggccctgggg	gtgcttctgc	agccttgaaa	3200
aagttgccct	tacctcctag	ggtcacctct	gctgccattc	tgagggaacat	3250

ctccaaggaa caggagggac tttggctaga gcctcctgcc tccccatctt 3300  
ctctctgccc agaggtcct gggcctggct tggctgtccc ctacctgtgt 3350  
ccccgggctg cacccttcc tcttctcttt ctctgtacag tctcagttgc 3400  
ttgctcttgt gcctcctggg caagggtga aggaggccac tccatctcac 3450  
ctcggggggc tgcctcaat gtgggagtga cccagccag atctgaagga 3500  
catttgggag agggatgccc aggaacgcct catctcagca gcctgggctc 3550  
ggcattccga agctgacttt ctataggcaa tttgtacct ttgtggagaa 3600  
atgtgtcacc tcccccaacc cgattcactc ttttctcctg ttttgtaaaa 3650  
aataaaaata aataataaca ataaaaaaa 3679

<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

Met	Arg	Leu	Leu	Val	Ala	Pro	Leu	Leu	Leu	Ala	Trp	Val	Ala	Gly	1	5	10	15
Ala	Thr	Ala	Thr	Val	Pro	Val	Val	Pro	Trp	His	Val	Pro	Cys	Pro	20	25	30	
Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser	35	40	45	
Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu	50	55	60	
Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu	65	70	75	
Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly	80	85	90	
Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe	95	100	105	
Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu	110	115	120	
Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His	125	130	135	
Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His	140	145	150	

104720-9567050

Asn	Gln	Leu	Tyr	Arg	Ile	Ala	Pro	Arg	Ala	Phe	Ser	Gly	Leu	Ser	155	160	165
Asn	Leu	Leu	Arg	Leu	His	Leu	Asn	Ser	Asn	Leu	Leu	Arg	Ala	Ile	170	175	180
Asp	Ser	Arg	Trp	Phe	Glu	Met	Leu	Pro	Asn	Leu	Glu	Ile	Leu	Met	185	190	195
Ile	Gly	Gly	Asn	Lys	Val	Asp	Ala	Ile	Leu	Asp	Met	Asn	Phe	Arg	200	205	210
Pro	Leu	Ala	Asn	Leu	Arg	Ser	Leu	Val	Leu	Ala	Gly	Met	Asn	Leu	215	220	225
Arg	Glu	Ile	Ser	Asp	Tyr	Ala	Leu	Glu	Gly	Leu	Gln	Ser	Leu	Glu	230	235	240
Ser	Leu	Ser	Phe	Tyr	Asp	Asn	Gln	Leu	Ala	Arg	Val	Pro	Arg	Arg	245	250	255
Ala	Leu	Glu	Gln	Val	Pro	Gly	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	260	265	270
Asn	Pro	Leu	Gln	Arg	Val	Gly	Pro	Gly	Asp	Phe	Ala	Asn	Met	Leu	275	280	285
His	Leu	Lys	Glu	Leu	Gly	Leu	Asn	Asn	Met	Glu	Glu	Leu	Val	Ser	290	295	300
Ile	Asp	Lys	Phe	Ala	Leu	Val	Asn	Leu	Pro	Glu	Leu	Thr	Lys	Leu	305	310	315
Asp	Ile	Thr	Asn	Asn	Pro	Arg	Leu	Ser	Phe	Ile	His	Pro	Arg	Ala	320	325	330
Phe	His	His	Leu	Pro	Gln	Met	Glu	Thr	Leu	Met	Leu	Asn	Asn	Asn	335	340	345
Ala	Leu	Ser	Ala	Leu	His	Gln	Gln	Thr	Val	Glu	Ser	Leu	Pro	Asn	350	355	360
Leu	Gln	Glu	Val	Gly	Leu	His	Gly	Asn	Pro	Ile	Arg	Cys	Asp	Cys	365	370	375
Val	Ile	Arg	Trp	Ala	Asn	Ala	Thr	Gly	Thr	Arg	Val	Arg	Phe	Ile	380	385	390
Glu	Pro	Gln	Ser	Thr	Leu	Cys	Ala	Glu	Pro	Pro	Asp	Leu	Gln	Arg	395	400	405
Leu	Pro	Val	Arg	Glu	Val	Pro	Phe	Arg	Glu	Met	Thr	Asp	His	Cys			

FOR "S670650"

410	415	420
Leu Pro Leu Ile Ser Pro Arg Ser Phe	Pro Pro Ser Leu Gln Val	
425	430	435
Ala Ser Gly Glu Ser Met Val Leu His	Cys Arg Ala Leu Ala Glu	
440	445	450
Pro Glu Pro Glu Ile Tyr Trp Val Thr	Pro Ala Gly Leu Arg Leu	
455	460	465
Thr Pro Ala His Ala Gly Arg Arg Tyr	Arg Val Tyr Pro Glu Gly	
470	475	480
Thr Leu Glu Leu Arg Arg Val Thr Ala	Glu Glu Ala Gly Leu Tyr	
485	490	495
Thr Cys Val Ala Gln Asn Leu Val Gly	Ala Asp Thr Lys Thr Val	
500	505	510
Ser Val Val Val Gly Arg Ala Leu Leu	Gln Pro Gly Arg Asp Glu	
515	520	525
Gly Gln Gly Leu Glu Leu Arg Val Gln	Glu Thr His Pro Tyr His	
530	535	540
Ile Leu Leu Ser Trp Val Thr Pro Pro	Asn Thr Val Ser Thr Asn	
545	550	555
Leu Thr Trp Ser Ser Ala Ser Ser Leu	Arg Gly Gln Gly Ala Thr	
560	565	570
Ala Leu Ala Arg Leu Pro Arg Gly Thr	His Ser Tyr Asn Ile Thr	
575	580	585
Arg Leu Leu Gln Ala Thr Glu Tyr Trp	Ala Cys Leu Gln Val Ala	
590	595	600
Phe Ala Asp Ala His Thr Gln Leu Ala	Cys Val Trp Ala Arg Thr	
605	610	615
Lys Glu Ala Thr Ser Cys His Arg Ala	Leu Gly Asp Arg Pro Gly	
620	625	630
Leu Ile Ala Ile Leu Ala Leu Ala Val	Leu Leu Leu Ala Ala Gly	
635	640	645
Leu Ala Ala His Leu Gly Thr Gly Gln	Pro Arg Lys Gly Val Gly	
650	655	660
Gly Arg Arg Pro Leu Pro Pro Ala Trp	Ala Phe Trp Gly Trp Ser	
665	670	675

1344-20-2940660

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp  
                                 680                                685                                690

Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu  
                                 695                                700                                705

Leu Pro Pro Leu Ser Gln Asn Ser  
                                 710

<210> 246

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

aacaaggtaa gatgccatcc tg 22

<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

aaacttgatc atggagacca gctc 24

<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45

<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

<400> 249

gcaagccaag gcgctgtttg agaaggtgaa gaagttccgg acccatgtgg 50

aggaggggga cattgtgtac cgcctctaca tgcggcagac catcatcaag 100

gtgatcaagt tcctcctcat catctgtctac accgtctact acgtgcacaa 150

catcaagttc gacgtggact gcaccgtgga cattgagagc ctgacgggct 200  
accgcaccta ccgctgtgcc cccccctgg ccacactctt caagatcctg 250  
gcgtccttct acatcagcct agtcactctt tacggcctca tctgcatgta 300  
cacactgtgg tggatgctac ggcgctccct caagaagtac tcgtttgagt 350  
cgatccgtga ggagagcagc tacagcgaca tccccgacgt caagaacgac 400  
ttcgccctca tgctgcacct cattgaccaa tacgaccgcg tctactccaa 450  
gcgcttcgcc gtcttctgtt cggaggtgag tgagaacaag ctgcggcagc 500  
tgaacctcaa caacgagtgg acgctggaca agctccggca gcggctcacc 550  
aagaacgcgc aggacaagct ggagctgcac ctgttcatgc tcagtggcat 600  
ccctgacact gtgtttgacc tgggtggagct ggaggtcctc aagctggagc 650  
tgatccccga cgtgaccatc ccgcccagca ttgccagct caccggcctc 700  
aaggagctgt ggctctacca cacagcggcc aagattgaag cgcttgcgt 750  
ggccttcttg cgcgagaacc tgcgggcgct gcacatcaag ttcaccgaca 800  
tcaaggagat cccgctgtgg atctatagcc tgaagacact ggaggagctg 850  
cacctgacgg gcaacctgag cgcggagaac aaccgctaca tcgtcatcga 900  
cgggctgcgg gagctcaaac gcctcaaggt gctgcggctc aagagcaacc 950  
taagcaagct gccacaggtg gtcacagatg tgggcgtgca cctgcagaag 1000  
ctgtccatca acaatgaggg caccaagctc atcgctctca acagcctcaa 1050  
gaagatggcg aacctgactg agctggagct gatccgctgc gacctggagc 1100  
gcacccccca ctccatcttc agcctccaca acctgcagga gattgacctc 1150  
aaggacaaca acctcaagac catcgaggag atcatcagct tccagcacct 1200  
gcaccgcctc acctgcctta agctgtggta caaccacatc gcctacatcc 1250  
ccatccagat cggcaacctc accaacctgg agcgctctta cctgaaccgc 1300  
aacaagatcg agaagatccc caccagctc ttctactgcc gcaagctgcg 1350  
ctacctggac ctcagccaca acaacctgac ctctctccct gccgacatcg 1400  
gcctcctgca gaacctccag aacctagcca tcacggccaa ccggategag 1450



acgctccctc cggagctctt ccagtgccgg aagctgcggg ccctgcacct 1500  
gggcaacaac gtgctgcagt cactgccctc caggggtgggc gagctgacca 1550  
acctgacgca gatcgagctg cggggcaacc ggctggagtg cctgcctgtg 1600  
gagctgggcg agtgcccact gctcaagcgc agcggcttgg tggaggagga 1650  
ggacctgttc aacacactgc caccgcaggt gaaggagcgg ctgtggaggg 1700  
ctgacaagga gcaggcctga gcgaggccgg cccagcacag caagcagcag 1750  
gaccgctgcc cagtcctcag gcccggaggg gcaggcctag cttctcccag 1800  
aactcccga cagccaggac agcctcgcgg ctgggcagga gcctggggcc 1850  
gcttgtagt caggccagag cgagaggaca gtatctgtgg ggctggcccc 1900  
ttttctccct ctgagactca cgtccccag ggcaagtgt tgtggaggag 1950  
agcaagtctc aagagcgcag tatttgata atcagggtct cctccctgga 2000  
ggccagctct gccccagggg ctgagctgcc accagaggtc ctgggacct 2050  
cactttagtt cttggtattt atttttctcc atctcccacc tccttcattc 2100  
agataactta tacattccca agaaagtcca gccagatgg aaggtgttca 2150  
gggaaaggtg ggctgccttt tcccctgtc cttatttagc gatgocgccg 2200  
ggcatttaac acccacctgg acttcagcag agtggtcgg ggccaaccag 2250  
ccatgggacg gtcaccagc agtgccgggc tgggctctgc ggtgcggctc 2300  
acgggagagc aggcctccag ctggaaaggc caggcctgga gcttgccctc 2350  
tcagtttttg tggcagtttt agttttttgt tttttttttt tttaatcaaa 2400  
aaacaatttt ttttaaaaaa aagctttgaa aatggatggt ttgggtatta 2450  
aaaagaaaaa aaaaacttaa aaaaaaaaag aactaacgg ccagtgaagt 2500  
ggagtctcag ggcagggtgg cagtttcct tgagcaaagc agccagacgt 2550  
tgaactgtgt ttcctttccc tgggcgcagg gtgcagggtg tcttcgggat 2600  
ctgggtgtgac cttggtccag gagttctatt tgttcctggg gagggaggtt 2650  
ttttgtttg ttttttgggt ttttttgggt tcttgttttc tttctcctcc 2700  
atgtgtcttg gcaggcactc atttctgtgg ctgtcgccca gagggaatgt 2750  
tctggagctg ccaaggaggg aggagactcg ggttggttaa tccccgatg 2800

aacggtgctc cattcgcacc tcccctcctc gtgcctgccc tgccctctcca 2850  
 cgcacagtgt taaggagcca agaggagcca cttcgcccag actttgtttc 2900  
 cccacctcct ggggcatggg tgtgtccagt gccaccgctg gcctccgctg 2950  
 cttccatcag cctgtcgcc acctggctct tcatgaagag cagacactta 3000  
 gaggctggtc ggggaatgggg aggtcgcccc tgggagggca ggcgttggtt 3050  
 ccaagccggt tcccgtcctt ggcgcctgga gtgcacacag cccagtcggc 3100  
 acctggtggc tggaagccaa cctgcttttag atcactcggg tccccacctt 3150  
 agaaggggtc ccgccttaga tcaatcacgt ggacactaag gcacgtttta 3200  
 gagtctcttg tcttaatgat tatgtccatc cgtctgtccg tccatttggtg 3250  
 ttttctgcgt cgtgtcattg gatataatcc tcagaaataa tgcacactag 3300  
 cctctgacaa ccatgaagca aaaatccggt acatgtgggt ctgaacttgt 3350  
 agactcggtc acagtatcaa ataaaatcta taacagaaaa aaaaaaaaaa 3400

a 3401

<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

Met	Arg	Gln	Thr	Ile	Ile	Lys	Val	Ile	Lys	Phe	Ile	Leu	Ile	Ile
1				5					10					15

Cys	Tyr	Thr	Val	Tyr	Tyr	Val	His	Asn	Ile	Lys	Phe	Asp	Val	Asp
				20					25					30

Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg
				35					40					45

Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe
				50					55					60

Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr
				65					70					75

Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu
				80					85					90

Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

CCDS:34660

	95		100		105
Asn Asp Phe Ala Phe Met Leu His Leu	Ile Asp Gln Tyr Asp Pro				
110	115				120
Leu Tyr Ser Lys Arg Phe Ala Val Phe	Leu Ser Glu Val Ser Glu				
125	130				135
Asn Lys Leu Arg Gln Leu Asn Leu Asn	Asn Glu Trp Thr Leu Asp				
140	145				150
Lys Leu Arg Gln Arg Leu Thr Lys Asn	Ala Gln Asp Lys Leu Glu				
155	160				165
Leu His Leu Phe Met Leu Ser Gly Ile	Pro Asp Thr Val Phe Asp				
170	175				180
Leu Val Glu Leu Glu Val Leu Lys Leu	Glu Leu Ile Pro Asp Val				
185	190				195
Thr Ile Pro Pro Ser Ile Ala Gln Leu	Thr Gly Leu Lys Glu Leu				
200	205				210
Trp Leu Tyr His Thr Ala Ala Lys Ile	Glu Ala Pro Ala Leu Ala				
215	220				225
Phe Leu Arg Glu Asn Leu Arg Ala Leu	His Ile Lys Phe Thr Asp				
230	235				240
Ile Lys Glu Ile Pro Leu Trp Ile Tyr	Ser Leu Lys Thr Leu Glu				
245	250				255
Glu Leu His Leu Thr Gly Asn Leu Ser	Ala Glu Asn Asn Arg Tyr				
260	265				270
Ile Val Ile Asp Gly Leu Arg Glu Leu	Lys Arg Leu Lys Val Leu				
275	280				285
Arg Leu Lys Ser Asn Leu Ser Lys Leu	Pro Gln Val Val Thr Asp				
290	295				300
Val Gly Val His Leu Gln Lys Leu Ser	Ile Asn Asn Glu Gly Thr				
305	310				315
Lys Leu Ile Val Leu Asn Ser Leu Lys	Lys Met Ala Asn Leu Thr				
320	325				330
Glu Leu Glu Leu Ile Arg Cys Asp Leu	Glu Arg Ile Pro His Ser				
335	340				345
Ile Phe Ser Leu His Asn Leu Gln Glu	Ile Asp Leu Lys Asp Asn				
350	355				360

For "964666"

Asn Leu Lys Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu His  
 365 370 375  
 Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile  
 380 385 390  
 Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu  
 395 400 405  
 Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys  
 410 415 420  
 Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe  
 425 430 435  
 Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala  
 440 445 450  
 Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln  
 455 460 465  
 Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln  
 470 475 480  
 Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile  
 485 490 495  
 Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly  
 500 505 510  
 Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp  
 515 520 525  
 Leu Phe Asn Thr Leu Pro Pro Glu Val Lys Glu Arg Leu Trp Arg  
 530 535 540  
 Ala Asp Lys Glu Gln Ala  
 545

<210> 251

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 251

caacaatgag ggcaccaagc 20

<210> 252

<211> 24

104120"95670660

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 252  
 gatggctagg ttctggaggt tctg 24

<210> 253  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 253  
 caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254  
 <211> 1650  
 <212> DNA  
 <213> Homo Sapien

<400> 254  
 gcctgttgct gatgctgccg tgcggtactt gtcattggagc tggcactgcg 50  
 gcgctctccc gtcccgcggt ggttgetgct gctgccgctg ctgctggggc 100  
 tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150  
 tgggattatg tgacgggtccg caaggatgcc tacatgttct ggtggctcta 200  
 ttatgccacc aactcctgca agaacttctc agaactgccc ctggtcattgt 250  
 ggcttcaggg cgggtccaggc ggttctagca ctggatttgg aaactttgag 300  
 gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctggct 350  
 ccaggctgcc agtctcctat ttgtggataa tcccgtgggc actgggttca 400  
 gttatgtgaa tggtagtggt gcctatgcca aggacctggc tatggtggct 450  
 tcagacatga tggttctcct gaagaccttc ttcagttgcc acaaagaatt 500  
 ccagacagtt ccattctaca ttttctcaga gtccatgga ggaaaaatgg 550  
 cagctggcat tggctagag ctttataagg ccattcagcg agggaccatc 600  
 aagtgcaact ttgcgggggt tgccttgggt gattcctgga tctccctgt 650  
 tgattcgggt ctctcctggg gaccttacct gtacagcatg tctcttctcg 700

Trp Pro Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val  
35 40 45

Arg	Lys	Asp	Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn	
				50					55					60	
Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln	
				65					70					75	
Gly	Gly	Pro	Gly	Gly	Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu	
				80					85					90	
Ile	Gly	Pro	Leu	Asp	Ser	Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp	
				95					100					105	
Leu	Gln	Ala	Ala	Ser	Leu	Leu	Phe	Val	Asp	Asn	Pro	Val	Gly	Thr	
				110					115					120	
Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly	Ala	Tyr	Ala	Lys	Asp	Leu	
				125					130					135	
Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe	
				140					145					150	
Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe	Tyr	Ile	Phe	Ser	
				155					160					165	
Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu	
				170					175					180	
Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly	
				185					190					195	
Val	Ala	Leu	Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	Val	Leu	
				200					205					210	
Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys	
				215					220					225	
Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala	
				230					235					240	
Val	Asn	Lys	Gly	Leu	Tyr	Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys	
				245					250					255	
Ala	Glu	Met	Ile	Ile	Glu	Gln	Asn	Thr	Asp	Gly	Val	Asn	Phe	Tyr	
				260					265					270	
Asn	Ile	Leu	Thr	Lys	Ser	Thr	Pro	Thr	Ser	Thr	Met	Glu	Ser	Ser	
				275					280					285	
Leu	Glu	Phe	Thr	Gln	Ser	His	Leu	Val	Cys	Leu	Cys	Gln	Arg	His	
				290					295					300	
Val	Arg	His	Leu	Gln	Arg	Asp	Ala	Leu	Ser	Gln	Leu	Met	Asn	Gly	

00004556-074404

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile	Pro Glu Asp Gln Ser Trp	
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val	Asn Met Glu Glu Asp Phe	
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp	Glu Leu Leu Glu Ala Gly	
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln	Leu Asp Leu Ile Val Asp	
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg	Lys Leu Lys Trp Pro Glu	
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp	Lys Ala Leu Tyr Ser Asp	
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe	Val Lys Ser Tyr Lys Asn	
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala	Gly His Met Val Pro Ser	
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met	Met Arg Leu Val Thr Gln	
440	445	450

Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

```

ggccgcggga gaggaggcca tgggcgcgcg cggggcgctg ctgctggcgc 50
tgctgctggc tcgggctgga ctcaggaagc cggagtcgca ggaggcggcg 100
ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150
tggagaggac gccgaactcg ggcgttgccc gtggcagggg agcctgcgcc 200
tgtgggattc ccacgtatgc ggagtgagec tgctcagcca ccgctgggca 250
ctcacggcgg cgcactgctt tgaaacctat agtgacctta gtgatccctc 300
cgggtggatg gtccagtttg gccagctgac ttccatgcca tccttctgga 350
gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400

```

1047203540660



cctcgctacc tggggaattc accctatgac attgccttgg tgaagctgtc 450  
 tgcacctgtc acctacacta aacacatcca gcccatctgt ctccaggcct 500  
 ccacatttga gtttgagaac cggacagact gctgggtgac tggctggggg 550  
 tacatcaaag aggatgaggc actgccatct cccacacccc tccaggaagt 600  
 tcaggtcgcc atcataaaca actctatgtg caaccacctc ttcctcaagt 650  
 acagtttccg caaggacatc tttggagaca tggtttgtgc tggcaacgcc 700  
 caaggcgaggga aggatgcctg cttcggtgac tcagggtggac ccttggcctg 750  
 taacaagaat ggactgtggt atcagattgg agtcgtgagc tggggagtgg 800  
 gctgtggtcg gcccaatcgg cccggtgtct acaccaatat cagccaccac 850  
 tttgagtgga tccagaagct gatggcccag agtggcatgt cccagccaga 900  
 cccctcctgg ccactactct tttccctct tctctgggt ctcctactcc 950  
 tggggccgggt ctgagcctac ctgagcccat gcagcctggg gccactgcca 1000  
 agtcaggccc tggttctctt ctgtcttgtt tggtaataaa cacattccag 1050  
 ttgatgcctt gcagggcatt cttcaaaaaa aaaaaaaaaa aaaaaaaaaa 1100

<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

Met	Gly	Ala	Arg	Gly	Ala	Leu	Leu	Leu	Ala	Leu	Leu	Leu	Ala	Arg
1				5					10					15

Ala	Gly	Leu	Arg	Lys	Pro	Glu	Ser	Gln	Glu	Ala	Ala	Pro	Leu	Ser
				20					25					30

Gly	Pro	Cys	Gly	Arg	Arg	Val	Ile	Thr	Ser	Arg	Ile	Val	Gly	Gly
			35						40					45

Glu	Asp	Ala	Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu	Arg
			50						55					60

Leu	Trp	Asp	Ser	His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg
			65						70					75

Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu
			80						85					90

104720354060

cccacgcgtc cgcggaacgcg tgggaagggc agaatgggac tccaagcctg 50

cctcctaggg ctctttgccc tcatectctc tggcaaattgc agttacagcc 100  
 cggagccccga ccagcggagg acgctgcccc caggctgggt gtccctgggc 150  
 cgtgcggacc ctgaggaaga gctgagtctc acctttgccc tgagacagca 200  
 gaatgtggaa agactctcgg agctggtgca ggctgtgtcg gatcccagct 250  
 ctctcaata cggaaaatac ctgaccctag agaattgtggc tgatctggtg 300  
 aggccatccc cactgaccct ccacacggtg caaaaatggc tcttggcagc 350  
 cggagcccag aagtgccatt ctgtgatcac acaggacttt ctgacttgct 400  
 ggctgagcat ccgacaagca gagctgctgc tccctggggc tgagtttcat 450  
 cactatgtgg gaggacctac ggaaacccat gttgtaaggc ccccatcc 500  
 ctaccagctt ccacaggcct tggcccccca tgtggacttt gtggggggac 550  
 tgcaccgttt tcccccaaca tcaccctga ggcaacgtcc tgagccgcag 600  
 gtgacaggga ctgtaggcct gcatctgggg gtaacccct ctgtgatccg 650  
 taagcgatac aacttgacct cacaagacgt gggctctggc accagcaata 700  
 acagccaagc ctgtgcccag ttctggagc agtatttcca tgactcagac 750  
 ctggctcagt tcattgcgct ctccggtggc aactttgcac atcaggcatc 800  
 agtagcccggt gtggttgagc aacaggggccg gggccgggcc gggattgagg 850  
 ccagtctaga tgtgcagtac ctgatgagtg ctggtgcca catctccacc 900  
 tgggtctaca gtagccctgg ccggcatgag ggacaggagc ccttcctgca 950  
 gtggctcatg ctgctcagta atgagtcagc cctgccacat gtgcatactg 1000  
 tgagctatgg agatgatgag gactccctca gcagcgcta catccagcgg 1050  
 gtcaaacactg agctcatgaa ggctgccgct cggggtctca cctgctctt 1100  
 cgctcaggt gacagtgggg ccgggtgttg gtctgtctct ggaagacacc 1150  
 agttccgccc taccttccct gcctccagcc cctatgtcac cacagtggga 1200  
 ggcacatcct tccaggaacc tttcctcatc acaaatgaaa ttgttgacta 1250  
 tatcagtgggt ggtggcttca gcaatgtgtt cccacggcct tcataccagg 1300  
 aggaagctgt aacgaagttc ctgagctcta gccccacct gccaccatcc 1350  
 agttacttca atgccagtgg ccgtgcctac ccagatgtgg ctgcactttc 1400

00004956-07449

tgatggctac tgggtggtca gcaacagagt gccattcca tgggtgtccg 1450  
 gaacctcggc ctctactcca gtgtttgggg ggatcctatc cttgatcaat 1500  
 gagcacagga tccttagtgg ccgccccctt cttggctttc tcaaccaag 1550  
 gctctaccag cagcatgggg caggtctctt tgatgtaacc cgtggctgcc 1600  
 atgagtcttg tctggatgaa gaggtagagg gccaggggtt ctgctctggt 1650  
 cctggctggg atcctgtaac aggtcgggga acaccaactt cccagctttg 1700  
 ctgaagactc tactcaaccc ctgacccttt cctatcagga gagatggctt 1750  
 gtccccctgcc ctgaagctgg cagttcagtc ccttattctg ccctgttggg 1800  
 agccctgctg aacctcaac tattgactgc tgcagacagc ttatctccct 1850  
 aacctgaaa tgctgtgagc ttgacttgac tccaaccct accatgctcc 1900  
 atcatactca ggtctcccta ctctgcctt agattcctca ataagatgct 1950  
 gtaactagca ttttttgaat gcctctccct ccgcatctca tctttctctt 2000  
 ttcaatcagg cttttccaaa gggttgtata cagactctgt gcactatttc 2050  
 acttgatatt cattcccaa ttcactgcaa ggagacctct actgtcaccg 2100  
 tttactcttt cctaccctga catccagaaa caatggcctc cagtgcatac 2150  
 ttctcaatct ttgctttatg gcctttccat catagttgcc cactccctct 2200  
 ccttacttag cttccaggtc ttaacttctc tgactactct tgtcttctc 2250  
 tctcatcaat ttctgcttct tcatggaatg ctgaccttca ttgctccatt 2300  
 tgtagatttt tgctcttctc agtttactca ttgtccctg gaacaaatca 2350  
 ctgacatcta caaccattac catctcacta aataagactt tctatccaat 2400  
 aatgattgat acctcaaag taaaaaa 2427

<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

Met	Gly	Leu	Gln	Ala	Cys	Leu	Leu	Gly	Leu	Phe	Ala	Leu	Ile	Leu
1					5				10				15	

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

090495-034

20	25	30
Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu		
35	40	45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg		
50	55	60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln		
65	70	75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg		
80	85	90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala		
95	100	105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu		
110	115	120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly		
125	130	135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val		
140	145	150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro		
155	160	165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser		
170	175	180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly		
185	190	195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn		
200	205	210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln		
215	220	225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu		
230	235	240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala		
245	250	255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly		
260	265	270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala		
275	280	285

for 35670660



Cys

&lt;210&gt; 260

&lt;211&gt; 1638

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 260

```

gccgcgcgct ctctcccggc gcccacacct gtctgagcgg cgcagcgagc 50
cgcgccccgg gcgggctgct cggcgcgga cagtgtcgg catggcaggg 100
attccagggc tcctcttctt tctcttcttt ctgctctgtg ctggtgggca 150
agtgagccct tacagtgcc cctggaaacc cacttgacct gcataccgcc 200
tcctgtcgt cttgccccag tctacctca atttagccaa gccagacttt 250
ggagccgaag ccaaattaga agtatcttct tcatgtggac ccagtggtca 300
taagggaact ccaactgcca cttacgaaga ggccaagcaa tatctgtctt 350
atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcatt 400
tacatctca gcagtagtgg agatggggcc caacaccgag actcaggggtc 450
ttcaggaaag tctcgaagga agcggcagat ttatggctat gacagcaggt 500
tcagcatttt tgggaaggac ttctgtctca actaccttt ctcaacatca 550
gtgaagtatt ccacgggctg caccggcacc ctggtggcag agaagcatgt 600
cctcacagct gccactgca tacacgatgg aaaaacctat gtgaaaggaa 650
cccagaagct tcgagtgggc ttctaaagc ccaagtttaa agatggtggt 700
cgaggggcca acgactccac ttcagccatg ccgagcaga tgaaatttca 750
gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaagggca 800
atgccaatga catcggcatg gattatgatt atgccctcct ggaactcaaa 850
aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctctgtctaa 900
gcagctgcca gggggcagaa ttcacttctc tggttatgac aatgaccgac 950
caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000
ttgctctacc agcaatgcga tgcccagcca ggggccagcg ggtctgggggt 1050
ctatgtgagg atgtggaaga gacagcagca gaagtgggag cgaaaaatta 1100

```

F0740-3564066

ttggcatttt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150  
 gatttcaacg tggctgtcag aatcactcct ctcaaatatg cccagatttg 1200  
 ctattggatt aaaggaaact acctggattg tagggagggg tgacacagtg 1250  
 ttccctcctg gcagcaatta agggctcttca tgttcttatt ttaggagagg 1300  
 ccaaattgtt ttttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgtg 1350  
 tgtgtgtaag gtgtcttata atcttttacc tatttcttac aattgcaaga 1400  
 tgactggctt tactatttga aaactgggtt gtgtatcata tcatatatca 1450  
 ttttaagcagt ttgaaggcat acttttgcac agaaataaaa aaaatactga 1500  
 tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgtttttg 1550  
 caaactttga tttttatttc atctgaactt gtttcaaaga tttatatata 1600  
 atatttggca tacaagagat atgaaaaaaaa aaaaaaaaa 1638

<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Phe	Leu	Leu
1				5					10					15

Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro
				20					25					30

Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr
				35					40					45

Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu
				50					55					60

Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu
				65					70					75

Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu
				80					85					90

Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile
				95					100					105

Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser
				110					115					120

L04720"35640660



Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser  
 125 130 135  
 Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe  
 140 145 150  
 Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val  
 155 160 165  
 Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly  
 170 175 180  
 Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu  
 185 190 195  
 Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr  
 200 205 210  
 Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys  
 215 220 225  
 Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp  
 230 235 240  
 Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro  
 245 250 255  
 His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys  
 260 265 270  
 Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp  
 275 280 285  
 Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu  
 290 295 300  
 Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala  
 305 310 315  
 Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln  
 320 325 330  
 Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp  
 335 340 345  
 Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg  
 350 355 360  
 Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly  
 365 370 375  
 Asn Tyr Leu Asp Cys Arg Glu Gly  
 380

125 130 135  
 140 145 150  
 155 160 165  
 170 175 180  
 185 190 195  
 200 205 210  
 215 220 225  
 230 235 240  
 245 250 255  
 260 265 270  
 275 280 285  
 290 295 300  
 305 310 315  
 320 325 330  
 335 340 345  
 350 355 360  
 365 370 375  
 380

<210> 262  
 <211> 1378  
 <212> DNA  
 <213> Homo Sapien

<400> 262  
 gcatcgccct gggctctctcg agcctgctgc ctgctcccc gccccaccag 50  
 ccatgggtggt ttctggagcg cccccagccc tgggtggggg ctgtctcggc 100  
 accttcacct ccctgctgct gctggcgctg acagccatcc tcaatgcggc 150  
 caggatacct gttccccag cctgtgggaa gcccagcag ctgaaccggg 200  
 ttgtgggagg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250  
 atccagaaga atgggaccca ccaactgcgc ggttctctgc tcaccagccg 300  
 ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaacct 350  
 acctgttctc tgtgctgctg ggggcctggc agctggggaa cctggctct 400  
 cgggtccaga aggtgggtgt tgccctgggtg gagccccacc ctgtgtattc 450  
 ctggaaggaa ggtgcctgtg cagacattgc cctgggtgcgt ctcgagcgct 500  
 ccatacagtt ctgagagcgg gtccctgccc tctgcctacc tgatgcctct 550  
 atccacctcc ctccaaacac ccaactgctg atctcaggct gggggagcat 600  
 ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650  
 ttccatcat cgactcggaa gtctgcagcc atctgtactg gcggggagca 700  
 ggacagggac ccatcactga ggacatgctg tgtgccggct acttgagggg 750  
 ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800  
 tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggctgt 850  
 gccgagcgca acaggccccg ggtctacatc agcctctctg cgcaccgctc 900  
 ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950  
 ggggtggggc cctcagggca ccgagccagg gctctggggc cgccgcgcgc 1000  
 tcctagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050  
 cacatctgga tctggatctg cggcggcctc gggcggtttc ccccgccgta 1100  
 aataggctca tctacctata cctctggggg cccggacggc tgctgcggaa 1150

104740-35640560

aggaaacccc ctccccgacc cgcccagcgg cctcaggccc ccctccaagg 1200  
 catcaggccc cgcccaacgg cctcatgtcc ccgccccac gacttccggc 1250  
 cccgcccccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300  
 ataggatttt gtaaccctgc ccacatatct tattttattcc tccaatttca 1350  
 ataaattatt tattctccaa aaaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu	1	5	10	15
Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu	20	25	30	
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln	35	40	45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu	50	55	60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys	65	70	75	
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	80	85	90	
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu	95	100	105	
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys	110	115	120	
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys	125	130	135	
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser	140	145	150	
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala	155	160	165	
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp	170	175	180	

RefSeq: S64066

```

Arg Ser
<210> 264
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 264
  gtccgcaagg atgcctacat gttc 24

<210> 265
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 265
  gcagaggtgt ctaagggtg 19

<210> 266
<211> 24

```

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 266  
 agctctagac caatgccagc ttcc 24

<210> 267  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 267  
 gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 268  
 ggggaattca ccctatgaca ttgcc 25

<210> 269  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 269  
 gaatgccctg caagcatcaa ctgg 24

<210> 270  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 270  
 gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 271  
gcggaagggc agaatgggac tccaag 26

<210> 272  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 272  
cagccctgcc acatgtgc 18

<210> 273  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 273  
tactgggtgg tcagcaac 18

<210> 274  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 274  
ggcgaagagc agggtgagac cccg 24

<210> 275  
<211> 45

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 275  
gcctcatcc tctctggcaa atgcagttac agcccgaggc ccgac 45

<210> 276  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 276  
gggcagggat tccagggctc c 21

<210> 277  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 277  
ggctatgaca gcaggttc 18

<210> 278  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 278  
tgacaatgac cgaccagg 18

<210> 279  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 279  
gcacgcatt gctggtagag caag 24

<210> 280  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280

ttacagtgcc ccctggaaac ccacttggcc tgcataccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281

cgtctcgagc gctccatata gttcccttgc ccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

tggaggggga gcgggatgct tgtctgggcg actccggggg cccctcatg 50

tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

ccctcagacc ctgcagaagc tgaagggttc tatcatcgac tcggaagtct 50

gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100

atgctgtgtg ccggtact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50

ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100



agatgaggag aaacgtttga tggaggagct gcacaacctc taccgggccc 150  
 aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200  
 ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250  
 caaggagcgc gggcgccgcg gcgagaatct gttcgccatc acagacgagg 300  
 gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350  
 tacaacctca gcgccgccac ctgcagccca ggccagatgt gcggccacta 400  
 cacgcagggtg gtatgggcca agacagagag gatcggtgtt ggttcccact 450  
 tctgtgagaa gctccagggt gttgaggaga ccaacatcga attactggtg 500  
 tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550  
 ggggactccg tgctcccaat gtccctctgg ctaccactgc aagaactccc 600  
 tctgtgaacc catcggaagc ccggaagatg ctcaggattt gccttacctg 650  
 gtaactgagg ccccatcctt ccgggcgact gaagcatcag actctaggaa 700  
 aatgggtact ctttcttccc tagcaacggg gattccggct ttcttggtaa 750  
 cagaggtctc aggtccctg gcaaccaagg ctctgcctgc tgtggaaacc 800  
 caggccccaa cttccttagc aacgaaagac ccgccctcca tggcaacaga 850  
 ggctccacct tgcgtaacaa ctgagggtccc ttccatcttg gcagctcaca 900  
 gcctgcctc cttggatgag gagccagtta cttccccaa atcgacccat 950  
 gttcctatcc caaaatcagc agacaaagtg acagacaaaa caaaagtgcc 1000  
 ctctaggagc ccagagaact ctctggaccc caagatgtcc ctgacagggg 1050  
 caaggggaact cctaccccat gccaggagg aggtgaggc tgaggctgag 1100  
 ttgcctcctt ccagttaggt cttggcctca gtttttccag ccaggacaa 1150  
 gccagggtgag ctgcaggcca cactggacca cacggggcac acctcctcca 1200  
 agtccctgcc caatttcccc aatacctctg ccaccgctaa tgccacgggt 1250  
 gggcgtgcc tggtctgca gtcgtccttg ccagggtcag agggccctga 1300  
 caagcctagc gttgtgtcag ggctgaactc gggccctggt catgtgtggg 1350  
 gccctctcct gggactactg ctctgcctc ctctggtgtt ggctggaatc 1400

ttctgaatgg gataccactc aaaggggtgaa gaggtcagct gtcctcctgt 1450  
 catcttcccc accctgtccc cagcccctaa acaagatact tcttggttaa 1500  
 ggccctccgg aagggaaagg ctacggggca tgtgcctcat cacaccatcc 1550  
 atcctggagg cacaaggcct ggctggctgc gagctcagga ggccgctga 1600  
 ggactgcaca ccgggcccac acctctctg cccctccctc ctgagtcctg 1650  
 ggggtgggag gatttgagg agctcactgc ctacctggcc tggggctgtc 1700  
 tgccacacaca gcatgtgcgc tctccctgag tgctgtgta gctggggatg 1750  
 gggattccta ggggcagatg aaggacaagc cccactggag tggggttctt 1800  
 tgagtggggg aggcaggac gagggaagga aagtaactcc tgactctcca 1850  
 ataaaaacct gtccaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu
1				5					10					15

Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp
				20					25					30

Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala
				35					40					45

Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp
				50					55					60

Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val
				65					70					75

Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe
				80					85					90

Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu
				95					100					105

Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys
				110					115					120

Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala
				125					130					135

F04T20-95640660

Lys	Thr	Glu	Arg	Ile	Gly	Cys	Gly	Ser	His	Phe	Cys	Glu	Lys	Leu	
				140					145					150	
Gln	Gly	Val	Glu	Glu	Thr	Asn	Ile	Glu	Leu	Leu	Val	Cys	Asn	Tyr	
				155					160					165	
Glu	Pro	Pro	Gly	Asn	Val	Lys	Gly	Lys	Arg	Pro	Tyr	Gln	Glu	Gly	
				170					175					180	
Thr	Pro	Cys	Ser	Gln	Cys	Pro	Ser	Gly	Tyr	His	Cys	Lys	Asn	Ser	
				185					190					195	
Leu	Cys	Glu	Pro	Ile	Gly	Ser	Pro	Glu	Asp	Ala	Gln	Asp	Leu	Pro	
				200					205					210	
Tyr	Leu	Val	Thr	Glu	Ala	Pro	Ser	Phe	Arg	Ala	Thr	Glu	Ala	Ser	
				215					220					225	
Asp	Ser	Arg	Lys	Met	Gly	Thr	Pro	Ser	Ser	Leu	Ala	Thr	Gly	Ile	
				230					235					240	
Pro	Ala	Phe	Leu	Val	Thr	Glu	Val	Ser	Gly	Ser	Leu	Ala	Thr	Lys	
				245					250					255	
Ala	Leu	Pro	Ala	Val	Glu	Thr	Gln	Ala	Pro	Thr	Ser	Leu	Ala	Thr	
				260					265					270	
Lys	Asp	Pro	Pro	Ser	Met	Ala	Thr	Glu	Ala	Pro	Pro	Cys	Val	Thr	
				275					280					285	
Thr	Glu	Val	Pro	Ser	Ile	Leu	Ala	Ala	His	Ser	Leu	Pro	Ser	Leu	
				290					295					300	
Asp	Glu	Glu	Pro	Val	Thr	Phe	Pro	Lys	Ser	Thr	His	Val	Pro	Ile	
				305					310					315	
Pro	Lys	Ser	Ala	Asp	Lys	Val	Thr	Asp	Lys	Thr	Lys	Val	Pro	Ser	
				320					325					330	
Arg	Ser	Pro	Glu	Asn	Ser	Leu	Asp	Pro	Lys	Met	Ser	Leu	Thr	Gly	
				335					340					345	
Ala	Arg	Glu	Leu	Leu	Pro	His	Ala	Gln	Glu	Glu	Ala	Glu	Ala	Glu	
				350					355					360	
Ala	Glu	Leu	Pro	Pro	Ser	Ser	Glu	Val	Leu	Ala	Ser	Val	Phe	Pro	
				365					370					375	
Ala	Gln	Asp	Lys	Pro	Gly	Glu	Leu	Gln	Ala	Thr	Leu	Asp	His	Thr	
				380					385					390	
Gly	His	Thr	Ser	Ser	Lys	Ser	Leu	Pro	Asn	Phe	Pro	Asn	Thr	Ser	
				395					400					405	

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser  
410 415 420

tcattctcca agttatgggtg gacgtacttc tgttgttctc cctctgcttg 100  
ctttttcaca ttagcagacc ggacttaagt cacaacagat tatctttcat 150  
caaggcaagt tccatgagcc accttcaaag ccttcgagaa gtgaaactga 200  
acaacaatga attggagacc attccaaatc tgggaccagt ctcggaat 250  
attacacttc tctccttggc tggaaacagg attggtgaaa tactccctga 300  
acatctgaaa gagtttcagt cccttgaaac tttggacctt agcagcaaca 350  
atatttcaga gctccaaact gcatttccag ccctacagct caaatatctg 400  
tatctcaaca gcaaccgagt cacatcaatg gaacctgggt attttgacaa 450  
tttgggccaac acactccttg tgttaaagct gaacaggaac cgaatctcag 500  
ctatcccacc caagatgttt aaactgcccc aactgcaaca tctcgaattg 550  
aaccgaaaca agattaaana thtagatgga ctgacattcc aaggccttgg 600  
tgctctgaag tctctgaaaa tgcaaagaaa tggagtaacg aaacttatgg 650  
atggagcttt ttgggggctg agcaacatgg aaattttgca gctggacat 700  
aacaacctaa cagagattac caaaggctgg ctttacggct tgctgatgct 750  
gcaggaactt catctcagcc aaaatgccat caacaggatc agccctgatg 800  
cctgggagtt ctgccagaag ctcagtgagc tggacctaac tttcaatcac 850  
ttatcaaggc tagatgattc aagcttcctt ggccctaagct tactaaatac 900  
actgcacatt gggaacaaca gagtcagcta cattgctgat tgtgccttcc 950  
gggggctttc cagtttaaag actttggatc tgaagaacaa tgaaatttcc 1000  
tggactattg aagacatgaa tgggtgcttc tctgggcttg acaaactgag 1050  
gcgactgata ctccaaggaa atcggatccg ttctattact aaaaaagcct 1100  
tacttggttt ggatgcattg gagcatctag acctgagtga caacgcaatc 1150  
atgtctttac aaggcaatgc attttcacaa atgaagaaac tgcaacaatt 1200  
gcattttaat acatcaagcc ttttgtgca ttgccagcta aaatggctcc 1250  
cacagtgggt ggcggaanaa aactttcaga gctttgtaaa tgccagttgt 1300  
gccatcctc agctgctaaa aggaagaagc atttttgctg ttagcccaga 1350

tggctttgtg tgtgatgatt ttcccaaacc ccagatcacg gttcagccag 1400  
 aaacacagtc ggcaataaaa ggttccaatt tgagtttcat ctgctcagct 1450  
 gccagcagca gtgattcccc aatgactttt gcttggaata aagacaatga 1500  
 actactgcat gatgctgaaa tggaaaatta tgcacacctc cgggcccag 1550  
 gtggcgaggt gatggagtat accaccatcc ttgggtgctg cgaggtggaa 1600  
 ttgcccagtg aggggaaata tcagtgtgtc atctccaatc actttgggtc 1650  
 atctactct gtcaaagcca agcttacagt aaatatgctt ccctcattca 1700  
 ccaagacccc catggatctc accatccgag ctggggccat ggcacgcttg 1750  
 gagtgtgctg ctgtggggca ccagccccc cagatagcct ggcagaagga 1800  
 tgggggcaca gacttcccag ctgcacggga gagacgcatg catgtgatgc 1850  
 ccgaggatga cgtgttcttt atcgtggatg tgaagataga ggacattggg 1900  
 gtatacagct gcacagctca gaacagtgc ggaagtattt cagcaaagtc 1950  
 aactctgact gtctagaaa caccatcatt ttgcgggcca ctgttggacc 2000  
 gaactgtaac caaggagaa acagccgtcc tacagtgcac tgctggagga 2050  
 agccctcccc ctaaactgaa ctggaccaa gatgatagcc cattggtggt 2100  
 aaccgagagg cacttttttg cagcaggcaa tcagcttctg attattgtgg 2150  
 actcagatgt cagtgatgct gggaaatata catgtgagat gtctaacc 2200  
 cttggcactg agagaggaaa cgtgcgcctc agtgtgatcc ccactccaac 2250  
 ctgcgactcc cctcagatga cagcccatc gttagacgat gacggatggg 2300  
 ccactgtggg tgtcgtgate atagcgtgg ttgtgtgtgt ggtgggcacg 2350  
 tcaactcgtgt ggggtggtcat catataccac acaaggcgga ggaatgaaga 2400  
 ttgcagcatt accaacacag atgagaccaa cttgccagca gatattccta 2450  
 gttatttgtc atctcaggga acgttagctg acaggcagga tgggtacgtg 2500  
 tcttcagaaa gtggaagcca ccaccagttt gtcacatctt caggtgctgg 2550  
 atttttctta ccacaacatg acagtagtgg gacctgcat attgacaata 2600  
 gcagtgaagc tgatgtggaa gctgccacag atctgttctt ttgtccgttt 2650  
 ttgggatcca caggccctat gtatttgaag ggaaatgtgt atggctcaga 2700

tccttttgaa acatatcata caggttgag tcctgaccca agaacagttt 2750  
 taatggacca ctatgagccc agttacataa agaaaaagga gtgctaccca 2800  
 tgttctcatc cttcagaaga atcctgcgaa cggagcttca gtaatatatc 2850  
 gtggccttca catgtgagga agctacttaa cactagttac tctcacaatg 2900  
 aaggacctgg aatgaaaaat ctgtgtctaa acaagtcctc tttagatttt 2950  
 agtgcaaadc cagagccagc gtcggttgcc tcgagtaatt ctttcatggg 3000  
 tacctttgga aaagctctca ggagacctca cctagatgcc tattcaagct 3050  
 ttggacagcc atcagattgt cagccaagag ctttttattt gaaagctcat 3100  
 tcttccccag acttggactc tgggtcagag gaagatggga aagaaaggac 3150  
 agattttcag gaagaaaatc acatttgtac ctttaaacag actttagaaa 3200  
 actacaggac tccaaatttt cagtcttatg acttggacac atagactgaa 3250  
 tgagacccaa ggaaaagctt aacatactac ctcaagtga cttttattta 3300  
 aaagagagag aatcttatgt tttttaaatg gagttatgaa ttttaaaagg 3350  
 ataaaaatgc tttatttata cagatgaacc aaaattacaa aaagttatga 3400  
 aaatttttat actgggaatg atgctcatat aagaatacct ttttaaacta 3450  
 tttttaact ttgttttatg caaaaaagta tcttacgtaa attaatgata 3500  
 taaatcatga ttattttatg tatttttata atgccagatt tctttttatg 3550  
 gaaaatgagt tactaaagca ttttaaataa tacctgcctt gtaccatttt 3600  
 ttaaatagaa gttacttcat tatattttgc acattatatt taataaaatg 3650  
 tgtcaatttg aa 3662

<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

Met	Val	Asp	Val	Leu	Leu	Leu	Phe	Ser	Leu	Cys	Leu	Leu	Phe	His
1				5					10				15	

Ile	Ser	Arg	Pro	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
				20				25						30

FOR 20 354060

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu	35	40	45
Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser	50	55	60
Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu	65	70	75
Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu	80	85	90
Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro	95	100	105
Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr	110	115	120
Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu	125	130	135
Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys	140	145	150
Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn	155	160	165
Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala	170	175	180
Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met	185	190	195
Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu	200	205	210
Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly	215	220	225
Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn	230	235	240
Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu	245	250	255
Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser	260	265	270
Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn	275	280	285
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser			

104120-954000



				290						295					300
Leu	Lys	Thr	Leu	Asp	Leu	Lys	Asn	Asn	Glu	Ile	Ser	Trp	Thr	Ile	
				305					310					315	
Glu	Asp	Met	Asn	Gly	Ala	Phe	Ser	Gly	Leu	Asp	Lys	Leu	Arg	Arg	
				320					325					330	
Leu	Ile	Leu	Gln	Gly	Asn	Arg	Ile	Arg	Ser	Ile	Thr	Lys	Lys	Ala	
				335					340					345	
Phe	Thr	Gly	Leu	Asp	Ala	Leu	Glu	His	Leu	Asp	Leu	Ser	Asp	Asn	
				350					355					360	
Ala	Ile	Met	Ser	Leu	Gln	Gly	Asn	Ala	Phe	Ser	Gln	Met	Lys	Lys	
				365					370					375	
Leu	Gln	Gln	Leu	His	Leu	Asn	Thr	Ser	Ser	Leu	Leu	Cys	Asp	Cys	
				380					385					390	
Gln	Leu	Lys	Trp	Leu	Pro	Gln	Trp	Val	Ala	Glu	Asn	Asn	Phe	Gln	
				395					400					405	
Ser	Phe	Val	Asn	Ala	Ser	Cys	Ala	His	Pro	Gln	Leu	Leu	Lys	Gly	
				410					415					420	
Arg	Ser	Ile	Phe	Ala	Val	Ser	Pro	Asp	Gly	Phe	Val	Cys	Asp	Asp	
				425					430					435	
Phe	Pro	Lys	Pro	Gln	Ile	Thr	Val	Gln	Pro	Glu	Thr	Gln	Ser	Ala	
				440					445					450	
Ile	Lys	Gly	Ser	Asn	Leu	Ser	Phe	Ile	Cys	Ser	Ala	Ala	Ser	Ser	
				455					460					465	
Ser	Asp	Ser	Pro	Met	Thr	Phe	Ala	Trp	Lys	Lys	Asp	Asn	Glu	Leu	
				470					475					480	
Leu	His	Asp	Ala	Glu	Met	Glu	Asn	Tyr	Ala	His	Leu	Arg	Ala	Gln	
				485					490					495	
Gly	Gly	Glu	Val	Met	Glu	Tyr	Thr	Thr	Ile	Leu	Arg	Leu	Arg	Glu	
				500					505					510	
Val	Glu	Phe	Ala	Ser	Glu	Gly	Lys	Tyr	Gln	Cys	Val	Ile	Ser	Asn	
				515					520					525	
His	Phe	Gly	Ser	Ser	Tyr	Ser	Val	Lys	Ala	Lys	Leu	Thr	Val	Asn	
				530					535					540	
Met	Leu	Pro	Ser	Phe	Thr	Lys	Thr	Pro	Met	Asp	Leu	Thr	Ile	Arg	
				545					550					555	

Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His	Pro
560	565		570
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe	Pro
575	580		585
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp	Val
590	595		600
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr	Ser
605	610		615
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala	Thr
620	625		630
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu	Asp
635	640		645
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile	Ala
650	655		660
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp	Ser
665	670		675
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn	Gln
680	685		690
Leu Leu Ile Ile	Val Asp Ser Asp Val	Ser Asp Ala Gly Lys	Tyr
695	700		705
Thr Cys Glu Met	Ser Asn Thr Leu Gly	Thr Glu Arg Gly Asn	Val
710	715		720
Arg Leu Ser Val	Ile Pro Thr Pro Thr	Cys Asp Ser Pro Gln	Met
725	730		735
Thr Ala Pro Ser	Leu Asp Asp Asp Gly	Trp Ala Thr Val Gly	Val
740	745		750
Val Ile Ile Ala	Val Val Cys Cys Val	Val Gly Thr Ser Leu	Val
755	760		765
Trp Val Val Ile	Ile Tyr His Thr Arg	Arg Arg Asn Glu Asp	Cys
770	775		780
Ser Ile Thr Asn	Thr Asp Glu Thr Asn	Leu Pro Ala Asp Ile	Pro
785	790		795
Ser Tyr Leu Ser	Ser Gln Gly Thr Leu	Ala Asp Arg Gln Asp	Gly
800	805		810

protein data bank

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser  
 815 820 825  
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
 830 835 840  
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
 845 850 855  
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
 860 865 870  
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His  
 875 880 885  
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
 890 895 900  
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His  
 905 910 915  
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
 920 925 930  
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
 935 940 945  
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu  
 950 955 960  
 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn  
 965 970 975  
 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu  
 980 985 990  
 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg  
 995 1000 1005  
 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
 1010 1015 1020  
 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn  
 1025 1030 1035  
 His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro  
 1040 1045 1050  
 Asn Phe Gln Ser Tyr Asp Leu Asp Thr  
 1055

&lt;210&gt; 291

&lt;211&gt; 2906

2904356 2744  
 204720 9564060

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 291

```

ggggagagga attgaccatg taaaaggaga cttttttttt tgggtggtggt 50
ggctgttggg tgccctgcaa aaatgaagga tgcaggacgc agctttctcc 100
tggaaccgaa cgcaatggat aaactgattg tgcaagagag aaggaagaac 150
gaagcttttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200
acacagggag cattcaagaa tgaaataaac cagagttaga cccgcggggg 250
ttggtgtggt ctgacataaa taaataatct taaagcagct gttcccctcc 300
ccacccccaa aaaaaaggat gattggaaat gaagaaccga ggattcacia 350
agaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400
gatatttttg gaatgaaaag tttggggcctt ttttagtaaa gttaaagaact 450
ggtgtggtgg tgttttcctt tctttttgaa tttcccacaa gaggagagga 500
aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgcg 550
gcagattgag gcattgattg ggggagagaa accagcagag cacagttgga 600
tttgtgccta tgttgactaa aattgacgga taattgcagt tggatttttc 650
ttcatcaacc tccttttttt taaattttta ttctttttgg tatcaagatc 700
atgcgttttc tcttgttcct aaccacctgg atttccatct ggatgttgct 750
gtgatcagtc tgaaatacaa ctgtttgaat tccagaagga ccaacaccag 800
ataaattatg aatgttgaac aagatgacct tacatccaca gcagataatg 850
ataggtccta ggtttaacag ggccctatct gacccctgc ttgtggtgct 900
gctggctctt caacttcttg tgggtggctgg tctggtgcgg gctcagacct 950
gcccttctgt gtgctcctgc agcaaccagt tcagcaaggt gatttgtggt 1000
cggaaaaacc tgcgtgaggt tccggatggc atctccacca acacacggct 1050
gctgaacctc catgagaacc aaatccagat catcaaagtg aacagcttca 1100
agcacttgag gcacttgaa atcctacagt tgagtaggaa ccatatcaga 1150
accattgaaa ttggggcctt caatggtctg gcgaacctca acactctgga 1200
actctttgac aatcgtctta ctaccatccc gaatggagct tttgtatact 1250

```

F04F20-9964066

tgtctaaact gaaggagctc tggttgcgaa acaaccccat tgaaagcatc 1300  
 ccttcttatg cttttaacag aattccttct ttgcgccgac tagacttagg 1350  
 ggaattgaaa agactttcat acatctcaga aggtgccttt gaaggtctgt 1400  
 ccaacttgag gtatttgaac cttgccatgt gcaaccttcg ggaaatccct 1450  
 aacctcacac cgctcataaa actagatgag ctggatcttt ctgggaatca 1500  
 tttatctgcc atcaggcctg gctctttcca gggtttgatg caccttcaaa 1550  
 aactgtggat gatacagtcc cagattcaag tgattgaacg gaatgccttt 1600  
 gacaaccttc agtcactagt ggagatcaac ctggcacaca ataactaac 1650  
 attactgcct catgacctct tcactccctt gcatcatcta gagcggatac 1700  
 atttacaatca caacccttgg aactgtaact gtgacatact gtggctcagc 1750  
 tgggtggataa aagacatggc ccctcgaac acagcttggt gtgcccgggtg 1800  
 taacactcct cccaatctaa aggggaggta cattggagag ctcgaccaga 1850  
 attacttcac atgctatgct ccggtgattg tggagcccc tgcagacctc 1900  
 aatgtcactg aaggcatggc agctgagctg aaatgtcggg cctccacatc 1950  
 cctgacatct gtatcttga ttactccaaa tggaacagtc atgacacatg 2000  
 gggcgtacaa agtgccgata gctgtgctca gtgatggtac gttaaatttc 2050  
 acaaagttaa ctgtgcaaga tacaggcatg tacacatgta tggtgagtaa 2100  
 ttccgttggg aataactactg cttcagccac cctgaatggt actgcagcaa 2150  
 ccactactcc tttctcttac ttttcaaccg tcacagtaga gactatggaa 2200  
 ccgtctcagg atgaggcacg gaccacagat aacaatgtgg gtcccactcc 2250  
 agtggctgac tgggagacca ccaatgtgac cacctctctc acaccacaga 2300  
 gcacaaggtc gacagagaaa accttcacca tcccagtgac tgatataaac 2350  
 agtgggatcc caggaattga tgaggatcatg aagactacca aaatcatcat 2400  
 tgggtgtttt gtggccatca cactcatggc tgcagtgatg ctggtcattt 2450  
 tctacaagat gaggaagcag caccatcggc aaaaccatca cgccccaaca 2500  
 aggactgttg aaattattaa tgtggatgat gagattacgg gagacacacc 2550

catggaaagc cacctgcccc tgccctgctat cgagcatgag cacctaaatc 2600  
 actataactc atacaaatct cccttcaacc acacaacaac agttaacaca 2650  
 ataaattcaa tacacagttc agtgcattgaa ccgttattga tccgaatgaa 2700  
 ctctaaagac aatgtacaag agactcaaatt ctaaaacatt tacagagtta 2750  
 caaaaaaaca acaatcaaaa aaaaagacag tttattaaaa atgacacaaa 2800  
 tgactgggct aaatctactg tttcaaaaaa gtgtctttac aaaaaaaca 2850  
 aaaagaaaag aaatttattt attaaaaatt ctattgtgat ctaaagcaga 2900  
 caaaaa 2906

<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

Met	Leu	Asn	Lys	Met	Thr	Leu	His	Pro	Gln	Gln	Ile	Met	Ile	Gly
1				5					10					15
Pro	Arg	Phe	Asn	Arg	Ala	Leu	Phe	Asp	Pro	Leu	Leu	Val	Val	Leu
				20					25					30
Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
				35					40					45
Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
				50					55					60
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
				65					70					75
Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
				80					85					90
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
				95					100					105
Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
				110					115					120
Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
				125					130					135
Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
				140					145					150
Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser

	155		160		165
Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly	170		175		180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly	185		190		195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg	200		205		210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp	215		220		225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln	230		235		240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile	245		250		255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val	260		265		270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp	275		280		285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His	290		295		300
Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp	305		310		315
Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys	320		325		330
Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp	335		340		345
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro	350		355		360
Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys	365		370		375
Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn	380		385		390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val	395		400		405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp	410		415		420

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr  
 425 430 435  
 Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro  
 440 445 450  
 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser  
 455 460 465  
 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro  
 470 475 480  
 Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro  
 485 490 495  
 Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr  
 500 505 510  
 Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr  
 515 520 525  
 Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala  
 530 535 540  
 Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His  
 545 550 555  
 Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn  
 560 565 570  
 Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu  
 575 580 585  
 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser  
 590 595 600  
 Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn  
 605 610 615  
 Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn  
 620 625 630  
 Ser Lys Asp Asn Val Gln Glu Thr Gln Ile  
 635 640

<210> 293

<211> 4053

<212> DNA

<213> Homo Sapien

<400> 293

agccgacgct gctcaagctg caactctgtt gcagttggca gttcttttcg 50



gtttccctcc tgctgtttgg gggcatgaaa gggcttcgcc gccgggagta 100  
aaagaaggaa ttgaccgggc agcgcgaggg aggagcgcgc acgcgaccgc 150  
gagggcgggc gtgcaccctc ggctggaagt ttgtgccggg ccccgagcgc 200  
gcgcgggctg ggagcttcgg gtagagacct aggccgctgg accgcgatga 250  
gcgcgccgag cctccgtgcg cgcgccgcgg ggttggggct gctgctgtgc 300  
gcggtgctgg ggcgcgctgg ccggtccgac agcggcggtc gcggggaact 350  
cgggcagccc tctggggtag ccgccgagcg cccatgcccc actacctgcc 400  
gctgcctcgg ggacctgctg gactgcagtc gtaagcggct agcgcgtctt 450  
cccgagccac tcccgtcctg ggtcgctcgg ctggacttaa gtcacaacag 500  
attatctttc atcaaggcaa gttccatgag ccaccttcaa agccttcgag 550  
aagtgaaact gaacaacaat gaattggaga ccattccaaa tctgggacca 600  
gtctcggcaa atattacact tctctccttg gctggaaaca ggattgttga 650  
aatactccct gaacatctga aagagtttca gtcccttgaa actttggacc 700  
ttagcagcaa caatatttca gagctccaaa ctgcatttcc agccctacag 750  
ctcaaatact tgtatctcaa cagcaaccga gtcacatcaa tggaacctgg 800  
gtattttgac aatttggcc aacacctcct tgtgttaaag ctgaacagga 850  
accgaatctc agctatccca cccaagatgt ttaaactgcc ccaactgcaa 900  
catctcgaat tgaaccgaaa caagattaaa aatgtagatg gactgacatt 950  
ccaaggcctt ggtgctctga agtctctgaa aatgcaaaga aatggagtaa 1000  
cgaaacttat ggatggagct ttttgggggc tgagcaacat ggaaattttg 1050  
cagctggacc ataacaacct aacagagatt accaaaggct ggctttacgg 1100  
cttgctgatg ctgcaggaac ttcactctcag ccaaaatgcc atcaacagga 1150  
tcagccctga tgccctgggag ttctgccaga agctcagtga gctggacctt 1200  
actttcaatc acttatcaag gttagatgat tcaagcttcc ttggcctaag 1250  
cttactaaat aactgcaca ttgggaacaa cagagtcagc tacattgctg 1300  
attgtgcctt ccgggggctt tccagtttaa agactttgga tctgaagaac 1350

aatgaaat	cttgactat	tgaagacatg	aatggtgctt	tctctgggct	1400
tgacaaactg	aggcgactga	tactccaagg	aatcggatc	cgttctatta	1450
ctaaaaaagc	cttcactgg	ttggatgcat	tggagcatct	agacctgagt	1500
gacaacgcaa	tcatgtcttt	acaaggcaat	gcattttcac	aatgaagaa	1550
actgcaacaa	ttgcatttaa	atacatcaag	ccttttgtgc	gattgccagc	1600
taaaatggct	cccacagtgg	gtggcgga	acaactttca	gagctttgta	1650
aatgccagtt	gtgcccattc	tcagctgcta	aaaggaagaa	gcatttttgc	1700
tgtagccca	gatggctttg	tgtgtgatga	ttttcccaa	cccagatca	1750
cggttcagcc	agaaacacag	tcggcaataa	aaggttccaa	tttgagtttc	1800
atctgctcag	ctgccagcag	cagtgattcc	ccaatgactt	ttgcttgga	1850
aaaagacaat	gaactactgc	atgatgctga	aatggaaaat	tatgcacacc	1900
tccgggcccc	aggtggcgag	gtgatggagt	ataccaccat	ccttcggctg	1950
cgcgaggtgg	aatttgccag	tgaggggaaa	tatcagtgtg	tcatctcaa	2000
tcactttggt	tcatcctact	ctgtcaaagc	caagcttaca	gtaaatatgc	2050
ttcctcatt	caccaagacc	cccattggatc	tcaccatccg	agctggggcc	2100
atggcacgct	tggagtgtgc	tgctgtgggg	caccagccc	cccagatagc	2150
ctggcagaag	gatgggggca	cagacttccc	agctgcacgg	gagagacgca	2200
tgcatgtgat	gcccgaggat	gacgtgttct	ttatcgtgga	tgtgaagata	2250
gaggacattg	gggtatacag	ctgcacagct	cagaacagtg	caggaagtat	2300
ttcagcaaat	gcaactctga	ctgtcctaga	aacaccatca	tttttgcggc	2350
cactgttgga	ccgaactgta	accaaggagg	aaacagccgt	cctacagtgc	2400
attgctggag	gaagccctcc	ccctaaactg	aactggacca	aagatgatag	2450
cccattggtg	gtaaccgaga	ggcacttttt	tgcagcaggc	aatcagcttc	2500
tgattattgt	ggactcagat	gtcagtgatg	ctgggaaata	cacatgtgag	2550
atgtctaaca	cccttggcac	tgagagagga	aacgtgcgcc	tcagtgtgat	2600
ccccactcca	acctgcgact	cccctcagat	gacagcccca	tcgttagacg	2650
atgacggatg	ggccactgtg	ggtgtcgtga	tcatagccgt	ggtttgctgt	2700

gtggtgggca cgtcactcgt gtgggtgggc atcatatacc acacaaggcg 2750  
 gaggaatgaa gattgcagca ttaccaacac agatgagacc aacttgccag 2800  
 cagatattcc tagttatttg tcatctcagg gaacgttage tgacaggcag 2850  
 gatgggtacg tgtcttcaga aagtggaagc caccaccagt ttgtcacatc 2900  
 ttcagggtgct ggatTTTTct taccacaaca tgacagtagt gggacctgcc 2950  
 atattgacaa tagcagtga gctgatgtgg aagctgccac agatctgttc 3000  
 ctttgtccgt ttttgggatc cacaggccct atgtatttga agggaaatgt 3050  
 gtatggctca gatccttttg aaacatatca tacaggttgc agtctgacc 3100  
 caagaacagt tttaatggac cactatgagc ccagttacat aaagaaaaag 3150  
 gagtgcacc catgttctca tcttcagaa gaatcctgcg aacggagctt 3200  
 cagtaatata tcgtggcctt cacatgtgag gaagctactt aacactagtt 3250  
 actctcacia tgaaggacct ggaatgaaaa atctgtgtct aaacaagtcc 3300  
 tctttagatt ttagtgcaaa tccagagcca gcgtcggttg cctcgagtaa 3350  
 ttctttcatg ggtacctttg gaaaagctct caggagacct cacctagatg 3400  
 cctattcaag ctttggacag ccacagatt gtcagccaag agccttttat 3450  
 ttgaaagctc attcttcccc agacttggac tctgggtcag aggaagatgg 3500  
 gaaagaaagg acagattttc aggaagaaaa tcacatttgt acctttaaac 3550  
 agactttaga aaactacagg actccaaatt ttcagtccta tgacttggac 3600  
 acatagactg aatgagacca aaggaaaagc ttaacatact acctcaagtg 3650  
 aacttttatt taaaagagag agaactttat gttttttaaa tggagttatg 3700  
 aattttaaaa ggataaaaat gctttattta tacagatgaa ccaaaattac 3750  
 aaaaagttat gaaaattttt atactgggaa tgatgctcat ataagaatac 3800  
 ctttttaaac tattttttta ctttgtttta tgcaaaaaag tatcttacgt 3850  
 aaattaatga tataaatcat gattatttta tgtattttta taatgccaga 3900  
 tttcttttta tggaaaatga gttactaaag catttttaaat aataacctgcc 3950  
 ttgtaccatt ttttaaatag aagtacttc attatatattt gcacattata 4000

tttaataaaaa tgtgtcaatt tgaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4050

aaa 4053

<210> 294

<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

Met	Ser	Ala	Pro	Ser	Leu	Arg	Ala	Arg	Ala	Ala	Gly	Leu	Gly	Leu
1				5					10					15

Leu	Leu	Cys	Ala	Val	Leu	Gly	Arg	Ala	Gly	Arg	Ser	Asp	Ser	Gly
				20					25					30

Gly	Arg	Gly	Glu	Leu	Gly	Gln	Pro	Ser	Gly	Val	Ala	Ala	Glu	Arg
				35					40					45

Pro	Cys	Pro	Thr	Thr	Cys	Arg	Cys	Leu	Gly	Asp	Leu	Leu	Asp	Cys
				50					55					60

Ser	Arg	Lys	Arg	Leu	Ala	Arg	Leu	Pro	Glu	Pro	Leu	Pro	Ser	Trp
				65					70					75

Val	Ala	Arg	Leu	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
				80					85					90

Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu
				95					100					105

Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser
				110					115					120

Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu
				125					130					135

Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu
				140					145					150

Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro
				155					160					165

Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr
				170					175					180

Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu
				185					190					195

Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys
				200					205					210

Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

for 20" 3540660

				215					220					225
Lys	Ile	Lys	Asn	Val 230	Asp	Gly	Leu	Thr	Phe 235	Gln	Gly	Leu	Gly	Ala 240
Leu	Lys	Ser	Leu	Lys 245	Met	Gln	Arg	Asn	Gly 250	Val	Thr	Lys	Leu	Met 255
Asp	Gly	Ala	Phe	Trp 260	Gly	Leu	Ser	Asn	Met 265	Glu	Ile	Leu	Gln	Leu 270
Asp	His	Asn	Asn	Leu 275	Thr	Glu	Ile	Thr	Lys 280	Gly	Trp	Leu	Tyr	Gly 285
Leu	Leu	Met	Leu	Gln 290	Glu	Leu	His	Leu	Ser 295	Gln	Asn	Ala	Ile	Asn 300
Arg	Ile	Ser	Pro	Asp 305	Ala	Trp	Glu	Phe	Cys 310	Gln	Lys	Leu	Ser	Glu 315
Leu	Asp	Leu	Thr	Phe 320	Asn	His	Leu	Ser	Arg 325	Leu	Asp	Asp	Ser	Ser 330
Phe	Leu	Gly	Leu	Ser 335	Leu	Leu	Asn	Thr	Leu 340	His	Ile	Gly	Asn	Asn 345
Arg	Val	Ser	Tyr	Ile 350	Ala	Asp	Cys	Ala	Phe 355	Arg	Gly	Leu	Ser	Ser 360
Leu	Lys	Thr	Leu	Asp 365	Leu	Lys	Asn	Asn	Glu 370	Ile	Ser	Trp	Thr	Ile 375
Glu	Asp	Met	Asn	Gly 380	Ala	Phe	Ser	Gly	Leu 385	Asp	Lys	Leu	Arg	Arg 390
Leu	Ile	Leu	Gln	Gly 395	Asn	Arg	Ile	Arg	Ser 400	Ile	Thr	Lys	Lys	Ala 405
Phe	Thr	Gly	Leu	Asp 410	Ala	Leu	Glu	His	Leu 415	Asp	Leu	Ser	Asp	Asn 420
Ala	Ile	Met	Ser	Leu 425	Gln	Gly	Asn	Ala	Phe 430	Ser	Gln	Met	Lys	Lys 435
Leu	Gln	Gln	Leu	His 440	Leu	Asn	Thr	Ser	Ser 445	Leu	Leu	Cys	Asp	Cys 450
Gln	Leu	Lys	Trp	Leu 455	Pro	Gln	Trp	Val	Ala 460	Glu	Asn	Asn	Phe	Gln 465
Ser	Phe	Val	Asn	Ala 470	Ser	Cys	Ala	His	Pro 475	Gln	Leu	Leu	Lys	Gly 480

Arg	Ser	Ile	Phe	Ala	Val	Ser	Pro	Asp	Gly	Phe	Val	Cys	Asp	Asp	485	490	495
Phe	Pro	Lys	Pro	Gln	Ile	Thr	Val	Gln	Pro	Glu	Thr	Gln	Ser	Ala	500	505	510
Ile	Lys	Gly	Ser	Asn	Leu	Ser	Phe	Ile	Cys	Ser	Ala	Ala	Ser	Ser	515	520	525
Ser	Asp	Ser	Pro	Met	Thr	Phe	Ala	Trp	Lys	Lys	Asp	Asn	Glu	Leu	530	535	540
Leu	His	Asp	Ala	Glu	Met	Glu	Asn	Tyr	Ala	His	Leu	Arg	Ala	Gln	545	550	555
Gly	Gly	Glu	Val	Met	Glu	Tyr	Thr	Thr	Ile	Leu	Arg	Leu	Arg	Glu	560	565	570
Val	Glu	Phe	Ala	Ser	Glu	Gly	Lys	Tyr	Gln	Cys	Val	Ile	Ser	Asn	575	580	585
His	Phe	Gly	Ser	Ser	Tyr	Ser	Val	Lys	Ala	Lys	Leu	Thr	Val	Asn	590	595	600
Met	Leu	Pro	Ser	Phe	Thr	Lys	Thr	Pro	Met	Asp	Leu	Thr	Ile	Arg	605	610	615
Ala	Gly	Ala	Met	Ala	Arg	Leu	Glu	Cys	Ala	Ala	Val	Gly	His	Pro	620	625	630
Ala	Pro	Gln	Ile	Ala	Trp	Gln	Lys	Asp	Gly	Gly	Thr	Asp	Phe	Pro	635	640	645
Ala	Ala	Arg	Glu	Arg	Arg	Met	His	Val	Met	Pro	Glu	Asp	Asp	Val	650	655	660
Phe	Phe	Ile	Val	Asp	Val	Lys	Ile	Glu	Asp	Ile	Gly	Val	Tyr	Ser	665	670	675
Cys	Thr	Ala	Gln	Asn	Ser	Ala	Gly	Ser	Ile	Ser	Ala	Asn	Ala	Thr	680	685	690
Leu	Thr	Val	Leu	Glu	Thr	Pro	Ser	Phe	Leu	Arg	Pro	Leu	Leu	Asp	695	700	705
Arg	Thr	Val	Thr	Lys	Gly	Glu	Thr	Ala	Val	Leu	Gln	Cys	Ile	Ala	710	715	720
Gly	Gly	Ser	Pro	Pro	Pro	Lys	Leu	Asn	Trp	Thr	Lys	Asp	Asp	Ser	725	730	735
Pro	Leu	Val	Val	Thr	Glu	Arg	His	Phe	Phe	Ala	Ala	Gly	Asn	Gln	740	745	750

Leu	Leu	Ile	Ile	Val	Asp	Ser	Asp	Val	Ser	Asp	Ala	Gly	Lys	Tyr
				755									760	765
Thr	Cys	Glu	Met	Ser	Asn	Thr	Leu	Gly	Thr	Glu	Arg	Gly	Asn	Val
				770									775	780
Arg	Leu	Ser	Val	Ile	Pro	Thr	Pro	Thr	Cys	Asp	Ser	Pro	Gln	Met
				785									790	795
Thr	Ala	Pro	Ser	Leu	Asp	Asp	Asp	Gly	Trp	Ala	Thr	Val	Gly	Val
				800									805	810
Val	Ile	Ile	Ala	Val	Val	Cys	Cys	Val	Val	Gly	Thr	Ser	Leu	Val
				815									820	825
Trp	Val	Val	Ile	Ile	Tyr	His	Thr	Arg	Arg	Arg	Asn	Glu	Asp	Cys
				830									835	840
Ser	Ile	Thr	Asn	Thr	Asp	Glu	Thr	Asn	Leu	Pro	Ala	Asp	Ile	Pro
				845									850	855
Ser	Tyr	Leu	Ser	Ser	Gln	Gly	Thr	Leu	Ala	Asp	Arg	Gln	Asp	Gly
				860									865	870
Tyr	Val	Ser	Ser	Glu	Ser	Gly	Ser	His	His	Gln	Phe	Val	Thr	Ser
				875									880	885
Ser	Gly	Ala	Gly	Phe	Phe	Leu	Pro	Gln	His	Asp	Ser	Ser	Gly	Thr
				890									895	900
Cys	His	Ile	Asp	Asn	Ser	Ser	Glu	Ala	Asp	Val	Glu	Ala	Ala	Thr
				905									910	915
Asp	Leu	Phe	Leu	Cys	Pro	Phe	Leu	Gly	Ser	Thr	Gly	Pro	Met	Tyr
				920									925	930
Leu	Lys	Gly	Asn	Val	Tyr	Gly	Ser	Asp	Pro	Phe	Glu	Thr	Tyr	His
				935									940	945
Thr	Gly	Cys	Ser	Pro	Asp	Pro	Arg	Thr	Val	Leu	Met	Asp	His	Tyr
				950									955	960
Glu	Pro	Ser	Tyr	Ile	Lys	Lys	Lys	Glu	Cys	Tyr	Pro	Cys	Ser	His
				965									970	975
Pro	Ser	Glu	Glu	Ser	Cys	Glu	Arg	Ser	Phe	Ser	Asn	Ile	Ser	Trp
				980									985	990
Pro	Ser	His	Val	Arg	Lys	Leu	Leu	Asn	Thr	Ser	Tyr	Ser	His	Asn
				995									1000	1005
Glu	Gly	Pro	Gly	Met	Lys	Asn	Leu	Cys	Leu	Asn	Lys	Ser	Ser	Leu

1010	1015	1020
Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn		
1025	1030	1035
Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu		
1040	1045	1050
Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg		
1055	1060	1065
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly		
1070	1075	1080
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn		
1085	1090	1095
His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro		
1100	1105	1110
Asn Phe Gln Ser Tyr Asp Leu Asp Thr		
1115		

&lt;210&gt; 295

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 295

ggaaccgaat ctcagcta 18

&lt;210&gt; 296

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 296

cctaaactga actggacca 19

&lt;210&gt; 297

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

1010 1015 1020  
 1025 1030 1035  
 1040 1045 1050  
 1055 1060 1065  
 1070 1075 1080  
 1085 1090 1095  
 1100 1105 1110  
 1115



<400> 297  
ggctggagac actgaacct 19

<210> 298  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 298  
acagctgcac agctcagaac agtg 24

<210> 299

<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 299  
cattcccagt ataaaaattt tc 22

<210> 300  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 300  
gggtcttggt gaatgagg 18

<210> 301  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 301  
gtgcctctcg gttaccacca atgg 24

<210> 302  
<211> 50  
<212> DNA  
<213> Artificial Sequence

0504955 07449

<220>

<223> Synthetic Oligonucleotide Probe

<400> 302

gcggccactg ttggaccgaa ctgtaaccaa gggagaaaca gccgtcctac 50

<210> 303

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 303

gcctttgaca accttcagtc actagtgg 28

<210> 304

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 304

cccatgtgt ccatgactgt tccc 24

<210> 305

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 305

tactgcctca tgacctcttc actcccttgc atcatcttag agcgg 45

<210> 306

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 306

actccaagga aatcgatcc gttc 24

<210> 307

<211> 24

104720-954060

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

ttagcagctg aggatgggca caac 24

<210> 308

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 308

actccaagga aatcggatcc gttc 24

<210> 309

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 309

gccttcactg gtttggatgc attggagcat ctagacctga gtgacaacgc 50

<210> 310

<211> 3296

<212> DNA

<213> Homo Sapien

<400> 310

caaaacttgc gtcgcgagga gcgcccagct tgacttgaat ggaaggagcc 50

cgagcccgcg gagcgagct gagactgggg gagcgcgctc ggcctgtggg 100

gcgccgctcg gcgccggggc gcagcaggga aggggaagct gtggtctgcc 150

ctgctccacg aggcgccact ggtgtgaacc gggagagccc ctgggtggtc 200

ccgtccccta tccctccttt atatagaaac cttccacact ggggaaggcag 250

cggcgaggca ggagggtca tggtagcaa ggaggccggc tgatctgcag 300

gcgcacagca ttccgagttt acagattttt acagatacca aatggaaggc 350

gaggaggcag aacagcctgc ctggttccat cagccctggc gcccaggcgc 400

atctgactcg gcacccctg caggcaccat ggcccagagc cgggtgctgc 450  
 tgctcctgct gctgctgccg ccacagctgc acctgggacc tgtgcttgcc 500  
 gtgagggccc caggatttgg ccgaagtggc ggccacagcc tgagccccga 550  
 agagaacgaa tttgcggagg aggagccggt gctggtactg agccctgagg 600  
 agcccggggc tggcccagcc gcggtcagct gccccgaga ctgtgcctgt 650  
 tcccaggagg gcgtcgtgga ctgtggcggt attgacctgc gtgagttccc 700  
 gggggacctg cctgagcaca ccaaccacct atctctgcag aacaaccage 750  
 tggaaaagat ctaccctgag gagctctccc ggctgcaccg gctggagaca 800  
 ctgaacctgc aaaacaaccg cctgacttcc cgagggtcc cagagaagge 850  
 gtttgagcat ctgaccaacc tcaattacct gtacttggcc aataacaage 900  
 tgaccttggc accccgcttc ctgccaaacg ccctgatcag tgtggacttt 950  
 gctgccaact atctcaccaa gatctatggg ctacaccttg gccagaagcc 1000  
 aaacttgagg tctgtgtacc tgcacaacaa caagctggca gacgccgggc 1050  
 tgccggacaa catgttcaac ggctccagca acgtcgaggt cctcatcctg 1100  
 tccagcaact tctgcgcca cgtgcccag cacctgccgc ctgccctgta 1150  
 caagctgcac ctcaagaaca acaagctgga gaagatcccc cggggggcct 1200  
 tcagcgagct gagcagcctg cgcgagctat acctgcagaa caactacctg 1250  
 actgacgagg gcttgacaa cgagaccttc tggaagctct ccagcctgga 1300  
 gtacctggat ctgtccagca acaacctgtc tcgggtccca gctgggctgc 1350  
 cgcgcagcct ggtgctgctg cacttgagga agaacgcat ccggagcgtg 1400  
 gacgcgaatg tgctgacccc catccgcagc ctggagtacc tgctgctgca 1450  
 cagcaaccag ctgcgggagc agggcatcca cccactggcc ttccagggcc 1500  
 tcaagcggtt gcacacggtg cacctgtaca acaacgcgct ggagcgcgtg 1550  
 cccagtggcc tgctcgccg cgtgcgcacc ctcatgatcc tgcacaacca 1600  
 gatcacagge attggccgcg aagactttgc caccacctac ttcttgagg 1650  
 agtcaacct cagctacaac cgcatacca gccacaggt gcaccgcgac 1700

090495 0740  
 104720 954020

gccttccgca agctgcgcct gctgcgctcg ctggacctgt cgggcaaccg 1750  
 gctgcacacg ctgccacctg ggctgcctcg aaatgtccat gtgctgaagg 1800  
 tcaagcgcaa tgagctggct gccttggcac gaggggcgct ggcgggcatg 1850  
 gctcagctgc gtgagctgta cctcaccagc aaccgactgc gcagccgagc 1900  
 cctgggcccc cgtgcctggg tggacctcgc ccattctgcag ctgctggaca 1950  
 tcgccgggaa tcagctcaca gagatccccg aggggctccc cgagtcactt 2000  
 gagtacctgt acctgcagaa caacaagatt agtgcggtgc ccgccaatgc 2050  
 cttcgactcc acgcccacc tcaaggggat ctttctcagg tttacaagc 2100  
 tggctgtggg ctccgtggtg gacagtgcct tccggaggct gaagcacctg 2150  
 caggtcttgg acattgaagg caacttagag tttggtgaca tttccaagga 2200  
 ccgtggccgc ttggggaagg aaaaggagga ggaggaagag gaggaggagg 2250  
 aggaagagga aacaagatag tgacaagggt atgcagatgt gacctaggat 2300  
 gatggaccgc cggactcttt tctgcagcac acgcctgtgt gctgtgagcc 2350  
 cccactctg ccgtgctcac acagacacac ccagctgcac acatgaggca 2400  
 tcccacatga cacgggctga cacagtctca tatccccacc cttccccacg 2450  
 gcgtgtccca cggccagaca catgcacaca catcacacc tcaaaccacc 2500  
 agctcagcca cacacaacta cctccaaac caccacagtc tctgtcacac 2550  
 cccactacc gctgccacgc cctctgaatc atgcagggaa gggctctgcc 2600  
 ctgcctggc acacacaggc acccattccc tccccctgct gacatgtgta 2650  
 tgcgtatgca tacacaccac acacacacac atgcacaagt catgtgcgaa 2700  
 cagccctcca aagcctatgc cacagacagc tcttgcccca gccagaatca 2750  
 gccatagcag ctgcgcgtct gccctgtcca tctgtccgtc cgttccctgg 2800  
 agaagacaca agggatatca tgctctgtgg ccagggtgct gccaccctct 2850  
 ggaactcaca aaagctggct ttatttctt tcccatccta tggggacagg 2900  
 agccttcagg actgctggcc tggcctggcc caccctgtc ctccagggtgc 2950  
 tgggcagtca ctctgctaag agtccctccc tgccacgccc tggcaggaca 3000  
 caggcacttt tccaatgggc aagcccagtg gaggcaggat gggagagccc 3050

000495 0744  
 104720 9564000

cctgggtgct gctggggcct tggggcagga gtgaagcaga ggtgatgggg 3100  
 ctgggctgag ccagggagga aggaccagc tgcacctagg agacaccttt 3150  
 gttcttcagg cctgtggggg aagttccggg tgcctttatt ttttattctt 3200  
 ttctaaggaa aaaaatgata aaaatctcaa agctgatttt tcttggtata 3250  
 gaaaaactaa tataaaagca ttatccctat ccctgcaaaa aaaaaa 3296

<210> 311  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 311  
 gcattggccg cgagactttg cc 22

<210> 312  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 312  
 gcggccacgg tccttggaat tg 22

<210> 313  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 313  
 tggaggagct caacctcagc tacaaccgca tcaccagccc acagg 45

<210> 314  
 <211> 3003  
 <212> DNA  
 <213> Homo Sapien

<400> 314  
 gggagggggc tccggggcgc gcgcagcaga cctgctccgg ccgcgcgcct 50  
 cgccgctgtc ctccgggagc ggcagcagta gcccgggcgg cgagggctgg 100

gggttctctcg	agactctcag	aggggcgcct	cccatcggcg	cccaccaccc	150
caacctgttc	ctcgcgcgcc	actgcgctgc	gccccaggac	ccgctgcca	200
acatggattt	tctcctggcg	ctggtgctgg	tatcctcgct	ctacctgcag	250
gcggccgcgcg	agttcgacgg	gaggtgccc	aggcaaatag	tgtcatcgat	300
tggcctatgt	cgttatggtg	ggaggattga	ctgctgctgg	ggctgggctc	350
gccagtcttg	gggacagtgt	cagcctgtgt	gccaaccacg	atgcaaacat	400
ggtgaatgta	tggggccaaa	caagtgcaag	tgtcatcctg	gttatgctgg	450
aaaaacctgt	aatcaagatc	taaatgagtg	tggcctgaag	ccccggccct	500
gtaagcacag	gtgcatgaac	acttacggca	gctacaagtg	ctactgtctc	550
aacggatata	tgctcatgcc	ggatggttcc	tgctcaagtg	ccctgacctg	600
ctccatggca	aactgtcagt	atggctgtga	tgttggtaaa	ggacaaatac	650
ggtgccagtg	cccatcccct	ggcctgcacc	tggctcctga	tgggaggacc	700
tgtgtagatg	ttgatgaatg	tgctacagga	agagcctcct	gccctagatt	750
taggcaatgt	gtcaacactt	ttgggagcta	catctgcaag	tgtcataaag	800
gcttcgatct	catgtatatt	ggaggcaaata	atcaatgtca	tgacatagac	850
gaatgctcac	ttggtcagta	tcagtgcagc	agctttgctc	gatgttataa	900
cgtacgtggg	tcctacaagt	gcaaatgtaa	agaaggatac	cagggtgatg	950
gactgacttg	tgtgtatatc	ccaaaagtta	tgattgaacc	ttcaggtcca	1000
attcatgtac	caaagggaaa	tggtaccatt	ttaaagggtg	acacaggaaa	1050
taataattgg	attcctgatg	ttggaagtac	ttggtggcct	ccgaagacac	1100
catatatctc	tcctatcatt	accaacaggc	ctacttctaa	gccaacaaca	1150
agacctacac	caaagccaac	accaattcct	actccaccac	caccaccacc	1200
cctgccaaaca	gagctcagaa	cacctctacc	acctacaacc	ccagaaaggc	1250
caaccaccgg	actgacaact	atagcaccag	ctgccagtac	acctccagga	1300
gggattacag	ttgacaacag	ggtacagaca	gaccctcaga	aaccagagg	1350
agatgtgttc	agtgttctgg	tacacagttg	taattttgac	catggacttt	1400

gtggatggat	cagggagaaa	gacaatgact	tgcactggga	accaatcagg	1450
gacccagcag	gtggacaata	tctgacagtg	tcggcagcca	aagccccagg	1500
gggaaaagct	gcacgcttgg	tgtacctct	cggccgcctc	atgcatttcag	1550
gggacctgtg	cctgtcattc	aggcacaagg	tgacggggct	gcactctggc	1600
acactccagg	tgtttgtgag	aaaacacggt	gccacaggag	cagccctgtg	1650
gggaagaaat	ggtggccatg	gctggaggca	aacacagatc	accttgcgag	1700
gggctgacat	caagagcgaa	tcacaaagat	gattaaaggg	ttggaaaaaa	1750
agatctatga	tggaaaatta	aaggaactgg	gattattgag	cctggagaag	1800
agaagactga	ggggcaaacc	attgatgggt	ttcaagtata	tgaagggttg	1850
gcacagagag	ggtggcgacc	agctgttctc	catatgcact	agaatagaa	1900
caagaggaaa	ctggcttaga	ctagagtata	agggagcatt	tcttggcagg	1950
ggccattggt	agaatacttc	ataaaaaaag	aagtgtgaaa	atctcagtat	2000
ctctctctct	ttctaaaaaa	ttagataaaa	atttgtctat	ttaagatggt	2050
taaagatggt	cttaccceaag	gaaaagtaac	aaattataga	atttcccaa	2100
agatgttttg	atcctactag	tagtatgcag	tgaaaatctt	tagaactaaa	2150
taatttggac	aaggcttaat	ttaggcattt	ccctcttgac	ctcctaattg	2200
agagggattg	aaaggggaag	agcccaccaa	atgctgagct	cactgaaata	2250
tctctccctt	atggcaatcc	tagcagtatt	aaagaaaaaa	ggaaactatt	2300
tattccaaat	gagagtatga	tggacagata	ttttagtatc	tcagtaatgt	2350
cctagtgtgg	cgggtggttt	caatgtttct	tcatggtaaa	ggtataagcc	2400
tttcatttgt	tcaatggatg	atgtttcaga	tttttttttt	tttaagagat	2450
ccttcaagga	acacagttca	gagagatttt	catcgggtgc	attctctctg	2500
cttcgtgtgt	gacaagttat	cttggtctgt	gagaaagagt	gccttgcccc	2550
acaccggcag	acctttcctt	cacctcatca	gtatgattca	gtttctctta	2600
tcaattggac	tctcccagg	tccacagaac	agtaatat	tttgaacaat	2650
aggtacaata	gaaggtcttc	tgtcatttaa	cctggtaaag	gcagggctgg	2700
agggggaaaa	taaatcatta	agcctttgag	taacggcaga	atatatggct	2750



gtagatccat ttttaatggt tcatttcctt tatggtcata taactgcaca 2800  
 gctgaagatg aaaggggaaa ataaatgaaa attttacttt tcgatgccaa 2850  
 tgatacattg cactaaactg atggaagaag ttatccaaag tactgtataa 2900  
 catcttgttt attatttaat gttttctaaa ataaaaaatg ttagtggttt 2950  
 tccaaatggc ctaataaaaa caattatttg taaataaaaa cactgttagt 3000  
 aat 3003

<210> 315

<211> 509

<212> PRT

<213> Homo Sapien

<400> 315

Met	Asp	Phe	Leu	Leu	Ala	Leu	Val	Leu	Val	Ser	Ser	Leu	Tyr	Leu	1	5	10	15
Gln	Ala	Ala	Ala	Glu	Phe	Asp	Gly	Arg	Trp	Pro	Arg	Gln	Ile	Val	20	25	30	
Ser	Ser	Ile	Gly	Leu	Cys	Arg	Tyr	Gly	Gly	Arg	Ile	Asp	Cys	Cys	35	40	45	
Trp	Gly	Trp	Ala	Arg	Gln	Ser	Trp	Gly	Gln	Cys	Gln	Pro	Val	Cys	50	55	60	
Gln	Pro	Arg	Cys	Lys	His	Gly	Glu	Cys	Ile	Gly	Pro	Asn	Lys	Cys	65	70	75	
Lys	Cys	His	Pro	Gly	Tyr	Ala	Gly	Lys	Thr	Cys	Asn	Gln	Asp	Leu	80	85	90	
Asn	Glu	Cys	Gly	Leu	Lys	Pro	Arg	Pro	Cys	Lys	His	Arg	Cys	Met	95	100	105	
Asn	Thr	Tyr	Gly	Ser	Tyr	Lys	Cys	Tyr	Cys	Leu	Asn	Gly	Tyr	Met	110	115	120	
Leu	Met	Pro	Asp	Gly	Ser	Cys	Ser	Ser	Ala	Leu	Thr	Cys	Ser	Met	125	130	135	
Ala	Asn	Cys	Gln	Tyr	Gly	Cys	Asp	Val	Val	Lys	Gly	Gln	Ile	Arg	140	145	150	
Cys	Gln	Cys	Pro	Ser	Pro	Gly	Leu	His	Leu	Ala	Pro	Asp	Gly	Arg	155	160	165	

164720"3564000

Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys	170	175	180
Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys	185	190	195
Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr	200	205	210
Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys	215	220	225
Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys	230	235	240
Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr	245	250	255
Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro	260	265	270
Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn	275	280	285
Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro	290	295	300
Tyr Ile Pro Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr	305	310	315
Thr Arg Pro Thr Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro Pro	320	325	330
Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr	335	340	345
Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala	350	355	360
Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln	365	370	375
Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ser Val Leu Val	380	385	390
His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu	395	400	405
Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly	410	415	420
Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys			

170 175 180  
 185 190 195  
 200 205 210  
 215 220 225  
 230 235 240  
 245 250 255  
 260 265 270  
 275 280 285  
 290 295 300  
 305 310 315  
 320 325 330  
 335 340 345  
 350 355 360  
 365 370 375  
 380 385 390  
 395 400 405  
 410 415 420



<400> 319

cttctttgaa aaggattatc acctgatcag gttctctctg catttgcccc 50  
tttagattgt gaaatgtggc tcaaggtctt cacaactttc ctttcctttg 100  
caacaggtgc ttgctcgggg ctgaaggtga cagtgccatc acacactgtc 150  
catggcgta gaggtcaggc cctctaccta cccgtccact atgggttcca 200  
cactccagca tcagacatcc agatcatatg gctatttgag agaccccaca 250  
caatgcccac atacttactg ggctctgtga ataagtctgt ggttcctgac 300  
ttggaatacc aacacaagtt caccatgatg ccacccaatg catctctgct 350  
tatcaaccca ctgcagttcc ctgatgaagg caattacatc gtgaagggtca 400  
acattcaggg aatggaact ctatctgcca gtcagaagat acaagtcacg 450  
gttgatgatc ctgtcacaaa gccagtgggtg cagattcatc ctccctctgg 500  
ggctgtggag tatgtgggga acatgacct gacatgccat gtggaagggg 550  
gcactcggct agcttaccaa tggctaaaaa atgggagacc tgtccacacc 600  
agctccacct actccttttc tccccaaaac aatacccttc atattgctcc 650  
agtaaccaag gaagacattg ggaattacag ctgcctgggtg aggaacctg 700  
tcagtgaat ggaaagtgat atcattatgc ccatcatata ttatggacct 750  
tatggacttc aagtgaattc tgataaaggg ctaaaagtag gggagtggt 800  
tactgttgac cttggagagg ccatectatt tgattgttct gctgattctc 850  
atccccccaa cacctactcc tggattagga ggactgacaa tactacatat 900  
atcattaagc atgggcctcg cttagaagtt gcacttgaga aagtagccca 950  
gaagacaatg gactatgtgt gctgtgctta caacaacata accggcaggc 1000  
aagatgaaac tcatttcaca gttatcatca cttccgtagg actggagaag 1050  
cttgcacaga aaggaaaatc attgtcacct ttagcaagta taactggaat 1100  
atcactatct ttgattatat ccatgtgtct tctcttccta tggaaaaaat 1150  
atcaacccta caaagttata aaacagaaac tagaaggcag gccagaaaca 1200  
gaatacagga aagctcaaac attttcaggc catgaagatg ctctggatga 1250

```
<210> 320
<211> 450
<212> PRT
<213> Homo Sapien
```

```

<400> 320
Met Trp Leu Lys Val Phe Thr Thr Phe Leu Ser Phe Ala Thr Gly
  1          5          10          15

Ala Cys Ser Gly Leu Lys Val Thr Val Pro Ser His Thr Val His
          20          25          30

Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe
          35          40          45

His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg
          50          55          60

```

Pro	His	Thr	Met	Pro	Lys	Tyr	Leu	Leu	Gly	Ser	Val	Asn	Lys	Ser	65	70	75
Val	Val	Pro	Asp	Leu	Glu	Tyr	Gln	His	Lys	Phe	Thr	Met	Met	Pro	80	85	90
Pro	Asn	Ala	Ser	Leu	Leu	Ile	Asn	Pro	Leu	Gln	Phe	Pro	Asp	Glu	95	100	105
Gly	Asn	Tyr	Ile	Val	Lys	Val	Asn	Ile	Gln	Gly	Asn	Gly	Thr	Leu	110	115	120
Ser	Ala	Ser	Gln	Lys	Ile	Gln	Val	Thr	Val	Asp	Asp	Pro	Val	Thr	125	130	135
Lys	Pro	Val	Val	Gln	Ile	His	Pro	Pro	Ser	Gly	Ala	Val	Glu	Tyr	140	145	150
Val	Gly	Asn	Met	Thr	Leu	Thr	Cys	His	Val	Glu	Gly	Gly	Thr	Arg	155	160	165
Leu	Ala	Tyr	Gln	Trp	Leu	Lys	Asn	Gly	Arg	Pro	Val	His	Thr	Ser	170	175	180
Ser	Thr	Tyr	Ser	Phe	Ser	Pro	Gln	Asn	Asn	Thr	Leu	His	Ile	Ala	185	190	195
Pro	Val	Thr	Lys	Glu	Asp	Ile	Gly	Asn	Tyr	Ser	Cys	Leu	Val	Arg	200	205	210
Asn	Pro	Val	Ser	Glu	Met	Glu	Ser	Asp	Ile	Ile	Met	Pro	Ile	Ile	215	220	225
Tyr	Tyr	Gly	Pro	Tyr	Gly	Leu	Gln	Val	Asn	Ser	Asp	Lys	Gly	Leu	230	235	240
Lys	Val	Gly	Glu	Val	Phe	Thr	Val	Asp	Leu	Gly	Glu	Ala	Ile	Leu	245	250	255
Phe	Asp	Cys	Ser	Ala	Asp	Ser	His	Pro	Pro	Asn	Thr	Tyr	Ser	Trp	260	265	270
Ile	Arg	Arg	Thr	Asp	Asn	Thr	Thr	Tyr	Ile	Ile	Lys	His	Gly	Pro	275	280	285
Arg	Leu	Glu	Val	Ala	Ser	Glu	Lys	Val	Ala	Gln	Lys	Thr	Met	Asp	290	295	300
Tyr	Val	Cys	Cys	Ala	Tyr	Asn	Asn	Ile	Thr	Gly	Arg	Gln	Asp	Glu	305	310	315
Thr	His	Phe	Thr	Val	Ile	Ile	Thr	Ser	Val	Gly	Leu	Glu	Lys	Leu			

320	325	330
Ala Gln Lys Gly Lys Ser Leu Ser Pro	Leu Ala Ser Ile Thr Gly	
335	340	345
Ile Ser Leu Phe Leu Ile Ile Ser Met	Cys Leu Leu Phe Leu Trp	
350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile	Lys Gln Lys Leu Glu Gly	
365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala	Gln Thr Phe Ser Gly His	
380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile	Tyr Glu Phe Val Ala Phe	
395	400	405
Pro Asp Val Ser Gly Val Ser Arg Ile	Pro Ser Arg Ser Val Pro	
410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp	Leu His Ser Thr Val Tyr	
425	430	435
Glu Val Ile Gln His Ile Pro Ala Gln	Gln Gln Asp His Pro Glu	
440	445	450

<210> 321  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 321  
 gatcctgtca caaagccagt ggtgc 25

<210> 322

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 322  
 cactgacagg gttcctcacc cagg 24

<210> 323  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 323

ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

&lt;210&gt; 324

&lt;211&gt; 2397

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 324

gcaagcggcg aaatggcgcc ctccgggagt cttgcagttc ccctggcagt 50  
cctggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100  
acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150  
tggatgatag aattttatgc cccgtggtgc cctgcttgct aaaatcttca 200  
accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250  
ttgcgaaagt agatgtcaca gagcagccag gactgagtgg acggtttatc 300  
ataactgctc ttcctactat ttatcattgt aaagatggtg aatttaggcg 350  
ctatcagggt ccaaggacta agaaggactt cataaacttt ataagtata 400  
aagagtggaa gagtattgag cccgtttcat catggtttgg tccaggttct 450  
gttctgatga gtagtatgtc agcactcttt cagctatcta tgtggatcag 500  
gacgtgccat aactacttta ttgaagacct tggattgcca gtgtggggat 550  
catatactgt ttttgcttta gcaactctgt tttccggact gttattagga 600  
ctctgtatga tatttgtggc agattgcctt tgtccttcaa aaaggcgcag 650  
accacagcca taccataacc cttcaaaaaa attattatca gaatctgcac 700  
aacctttgaa aaaagtggag gaggaacaag aggcggatga agaagatgtt 750  
tcagaagaag aagctgaaag taaagaagga acaaacaag actttccaca 800  
gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850  
cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900  
aagattgatc attttgtttg gtttgaagtg aactgtgact tttttgaata 950  
ttgcagggtt cagtctagat tgtcattaaa ttgaagagtc tacattcaga 1000

F04720"35640660



acataaaaagc actaggtata caagtttgaa atatgattta agcacagtat 1050  
 gatggtttaa atagttctct aatttttgaa aaatcgtgcc aagcaataag 1100  
 atttatgtat atttgtttaa taataaccta tttcaagtct gagttttgaa 1150  
 aatttacatt tcccaagtat tgcattattg aggtatttaa gaagattatt 1200  
 ttagagaaaa atatttctca tttgatataa ttttctctg tttcactgtg 1250  
 tgaaaaaaag aagatatttc ccataaatgg gaagtttgcc cattgtctca 1300  
 agaaatgtgt atttcagtga caatttcgtg gtcttttttag aggtatattc 1350  
 caaaatttcc ttgtattttt aggttatgca actaataaaa actaccttac 1400  
 attaattaat tacagttttc tacacatggg aatacaggat atgctactga 1450  
 tttaggaagt ttttaagttc atggatttct cttgattcca acaaagtttg 1500  
 attttctctt gtatttttct tacttactat gggttacatt ttttattttt 1550  
 caaattggat gataatttct tggaaacatt ttttatgttt tagtaaacag 1600  
 tatttttttg ttgtttcaaa ctgaagttta ctgagagatc catcaaattg 1650  
 aacaatctgt tgtaatttaa aattttggcc acttttttca gattttacat 1700  
 cattcttgct gaacttcaac ttgaaattgt ttttttttcc tttttggatg 1750  
 tgaagtgaa cattcctgat ttttgtctga tgtgaaaaag ccttggtatt 1800  
 ttacattttg aaaattcaaa gaagcttaat ataaaagttt gcattctact 1850  
 caggaaaaag catcttcttg tatatgtctt aaatgtattt ttgtcctcat 1900  
 atacagaaag ttcttaattg attttacagt ctgtaatgct tgatgtttta 1950  
 aaataataac atttttatat tttttaaaag acaaacttca tattatcctg 2000  
 tgttctttcc tgactggtaa tattgtgtgg gatttcacag gtaaaagtca 2050  
 gtaggatgga acattttagt gtatttttac tccttaaaga gctagaatac 2100  
 atagttttca ccttaaaaga agggggaaaa tcataaatac aatgaatcaa 2150  
 ctgaccatta cgtagtagac aatttctgta atgtcccctt ctttctaggc 2200  
 tctgttgctg tgtgaatcca ttagatttac agtatcgtaa tatacaagtt 2250  
 ttcttttaaag ccctctcctt tagaatttaa aatattgtac cattaaagag 2300  
 tttggatgtg taacttgtga tgccttagaa aaatataccta agcacaaaat 2350

090496-0740  
 104720-994050

<210>	325
<211>	280
<212>	PRT

<400> 325

Leu Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn  
20 25 30

Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln  
50 55 60

Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly  
80 85 90

Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys  
110 115 120

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser  
140 145 150

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser  
170 175 180

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys  
200 205 210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu

	215		220		225									
Ser	Glu	Ser	Ala	Gln	Pro	Leu	Lys	Lys	Val	Glu	Glu	Glu	Gln	Glu
				230					235					240
Ala	Asp	Glu	Glu	Asp	Val	Ser	Glu	Glu	Glu	Ala	Glu	Ser	Lys	Glu
				245					250					255
Gly	Thr	Asn	Lys	Asp	Phe	Pro	Gln	Asn	Ala	Ile	Arg	Gln	Arg	Ser
				260					265					270
Leu	Gly	Pro	Ser	Leu	Ala	Thr	Asp	Lys	Ser					
				275					280					

&lt;210&gt; 326

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 326

tgaggtgggc aagcggcgaa atg 23

&lt;210&gt; 327

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 327

tatgtggatc aggacgtgcc 20

&lt;210&gt; 328

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 328

tgcaggggttc agtctagatt g 21

&lt;210&gt; 329

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

for 20" 3340660

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 329  
 ttgaaggaca aaggcaatct gccac 25

<210> 330  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 330  
 ggagtcttgc agttcccctg gcagtcctgg tgctgttgct ttggg 45

<210> 331  
 <211> 2168  
 <212> DNA  
 <213> Homo Sapien

<400> 331  
 gcgagtgtcc agctgcggag acccgtgata attcgttaac taattcaaca 50  
 aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taaccagtg 100  
 ggacaggcgg attggaagag cgggaaggtc ctggcccaga gcagtgtgac 150  
 acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200  
 ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250  
 cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300  
 agagtacatc cttgtggagg aagccaagct ttccaagatt aagagctggg 350  
 ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400  
 tacctggctc accctgtgaa tgccatacaa ctggtgaagc ggctaaacac 450  
 agactggcct gcgctggagg accttgtcct gcaggactca gctgcaggtt 500  
 ttatcgccaa cctctctgtg cagcggcagt tcttccccac tgatgaggac 550  
 gagataggag ctgccaaagc cctgatgaga cttcaggaca catacaggct 600  
 ggaccagggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650  
 caatgctgag tgtggatgac tgctttggga tgggccgctc ggccatacat 700  
 gaaggggact attatcatac ggtgttgtgg atggagcagg tgctaaagca 750

2025-09-24 10:00:00

gcttgatgcc ggggaggagg ccaccacaac caagtcacag gtgctggact 800  
acctcagcta tgctgtcttc cagttgggtg atctgcaccg tgccctggag 850  
ctcaccgcgc gcttgccttc ccttgacca agccacgaac gagctggagg 900  
gaatctgcgg tactttgagc agttattgga ggaagagaga gaaaaaacgt 950  
taacaaatca gacagaagct gagctagcaa cccagaagg catctatgag 1000  
aggcctgtgg actacctgcc tgagagggat gtttacgaga gcctctgtcg 1050  
tggggagggg gtcaaaactga cccccgtag acagaagagg cttttctgta 1100  
ggtaccacca tggcaacagg gccccacagc tgctcattgc ccccttcaa 1150  
gaggaggacg agtgggacag cccgcacatc gtcagggtact acgatgtcat 1200  
gtctgatgag gaaatcgaga ggatcaagga gatcgcaaaa cctaaacttg 1250  
cacgagccac cgttcgtgat cccaagacag gagtccctac tgtcgccagc 1300  
taccgggttt ccaaaagctc ctggctagag gaagatgatg accctgttgt 1350  
ggcccgagta aatcgtcgga tgcagcatat cacagggtta acagtaaaga 1400  
ctgcagaatt gttacaggtt gcaaattatg gagtgggagg acagtatgaa 1450  
ccgcacttcg acttctctag gcgacctttt gacagcggcc tcaaacaga 1500  
ggggaatagg ttagcgacgt ttcttaacta catgagtgat gtagaagctg 1550  
gtggtgccac cgtcttccct gatctggggg ctgcaatttg gcctaagaag 1600  
ggtacagctg tgttctggta caacctcttg cggagcgggg aaggtgacta 1650  
ccgaacaaga catgtgcct gccctgtgct tgtgggctgc aagtgggtct 1700  
ccaataagtg gttccatgaa cgaggacagg agttcttgag accttggtga 1750  
tcaacagaag ttgactgaca tcttttctg tcttccct tcttggtcct 1800  
tcagcccatg tcaacgtgac agacacctt gtatgttctt ttgtatgttc 1850  
ctatcagget gatttttggg gaaatgaatg tttgtctgga gcagagggag 1900  
accatactag ggcgactcct gtgtgactga agtcccagcc cttccattca 1950  
gcctgtgcca tccctggccc caaggctagg atcaaagtgg ctgcagcaga 2000  
gttagctgtc tagcgctag caagggtgct ttgtacctca ggtgttttag 2050  
gtgtgagatg tttcagtga ccaaagttct gataccttgt ttacatgttt 2100

00495-040  
"9540000"

gtttttatgg catttctatc tattgtggct ttaccaaaaa ataaaaatgtc 2150

cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

Met	Lys	Leu	Trp	Val	Ser	Ala	Leu	Leu	Met	Ala	Trp	Phe	Gly	Val
1				5					10					15
Leu	Ser	Cys	Val	Gln	Ala	Glu	Phe	Phe	Thr	Ser	Ile	Gly	His	Met
				20					25					30
Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Lys	Glu	Leu	Val	Gln	Ser	Leu	Lys
				35					40					45
Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser
				50					55					60
Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp
				65					70					75
Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val
				80					85					90
Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu
				95					100					105
Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg
				110					115					120
Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala
				125					130					135
Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile
				140					145					150
Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser
				155					160					165
Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly
				170					175					180
Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln
				185					190					195
Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Thr	Lys	Ser	Gln	Val	Leu
				200					205					210

total 990660

Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg  
 215 220 225  
 Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His  
 230 235 240  
 Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu  
 245 250 255  
 Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu  
 260 265 270  
 Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro  
 275 280 285  
 Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys  
 290 295 300  
 Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His  
 305 310 315  
 Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu  
 320 325 330  
 Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met  
 335 340 345  
 Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys  
 350 355 360  
 Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr  
 365 370 375  
 Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp  
 380 385 390  
 Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile  
 395 400 405  
 Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn  
 410 415 420  
 Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg  
 425 430 435  
 Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala  
 440 445 450  
 Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr  
 455 460 465  
 Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr  
 470 475 480

090456 0440  
 104720 99670560

```

<210> 333
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 333
ccaggcacaa tttccaga 18

<210> 334
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 334
ggacccttct gtgtgccag 19

<210> 335
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 335
ggtctcaaga actoctgtc 19

<210> 336
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

```



<400> 336  
acactcagca ttgcctggta cttg 24

<210> 337  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 337  
gggcacatga ctgacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338  
<211> 2789

<212> DNA  
<213> Homo Sapien

<400> 338  
gcagtattga gttttacttc ctctctttt tagtggaaga cagaccataa 50  
tcccagtggt agtgaaattg attgtttcat ttattaccgt tttggctggg 100  
ggttagttcc gacaccttca cagttgaaga gcaggcagaa ggagttgtga 150  
agacaggaca atcttcttgg ggatgctggt cctggaagcc agcgggcctt 200  
gctctgtctt tggcctcatt gaccccaggt tctctggta aaactgaaag 250  
cctactactg gcctggtgcc catcaatcca ttgatccttg aggctgtgcc 300  
cctggggcac ccacctggca gggcctacca ccatgcgact gagctccctg 350  
ttggctctgc tgcggccagc gcttcccctc atcttagggc tgtctctggg 400  
gtgcagcctg agcctcctgc gggtttcctg gatccagggg gagggagaag 450  
atccctgtgt cgaggctgta ggggagcgag gagggccaca gaatccagat 500  
tcgagagctc ggctagacca aagtgatgaa gacttcaaac cccggattgt 550  
cccctactac agggacccca acaagcccta caagaaggtg ctcaggactc 600  
ggtacatcca gacagagctg ggctcccggt agcgggttget ggtggctgtc 650  
ctgacctccc gagctacact gtccactttg gccgtggctg tgaaccgtac 700  
ggtggcccat cacttccctc ggttactcta cttcactggg cagcgggggg 750  
cccgggctcc agcagggatg caggtggtgt ctcatgggga tgagcgggcc 800

For "994000" 041620

gcctggctca	tgtcagagac	cctgcgccac	cttcacacac	actttggggc	850
cgactacgac	tggttcttca	tcatgcagga	tgacacatat	gtgcaggccc	900
cccgcctggc	agcccttget	ggccacctca	gcataacca	agacctgtac	950
ttaggccggg	cagaggagtt	cattggcgca	ggcgagcagg	cccgtactg	1000
tcatgggggc	tttggctacc	tgttgtcacg	gagtctcctg	cttcgtctgc	1050
ggccacatct	ggatggctgc	cgaggagaca	ttctcagtgc	ccgtcctgac	1100
gagtggcttg	gacgctgcct	cattgactct	ctgggcgtcg	gctgtgtctc	1150
acagcaccag	gggcagcagt	atcgctcatt	tgaactggcc	aaaaataggg	1200
accctgagaa	ggaagggagc	tcggttttcc	tgagtgcctt	cgccgtgcac	1250
cctgtctccg	aaggtaccct	catgtaccgg	ctccacaaac	gcttcagcgc	1300
tctggagttg	gagcgggctt	acagtgaaat	agaacaactg	caggctcaga	1350
tccggaacct	gaccgtgctg	acccccgaag	gggaggcagg	gctgagctgg	1400
cccgttgggc	tccctgctcc	tttcacacca	cactctcgct	ttgaggtgct	1450
gggctgggac	tacttcacag	agcagcacac	cttctcctgt	gcagatgggg	1500
ctcccaagtg	cccactacag	ggggctagca	gggcggacgt	gggtgatgcg	1550
ttggagactg	ccctggagca	gctcaatcgg	cgctatcagc	cccgcctgcg	1600
cttccagaag	cagcgactgc	tcaacggcta	tcggcgcttc	gaccagcac	1650
ggggcatgga	gtacaccctg	gacctgctgt	tggaatgtgt	gacacagcgt	1700
gggcaccggc	gggccttggc	tcgcagggtc	agcctgctgc	ggccactgag	1750
ccgggtggaa	atcctacctt	tgccttatgt	cactgaggcc	acccgagtgc	1800
agctgggtgct	gccactcctg	gtggctgaag	ctgctgcagc	cccggctttc	1850
ctcgaggcgt	ttgcagccaa	tgtcctggag	ccacgagaac	atgcattgct	1900
caccctgttg	ctggtctacg	ggccacgaga	aggtggccgt	ggagctccag	1950
accattttct	tgggggtgaag	gctgcagcag	cggagttaga	gcgacggtac	2000
cctgggacga	ggctggcctg	gctcgctgtg	cgagcagagg	ccccttccca	2050
ggtgcgactc	atggacgtgg	tctcgaagaa	gcacctgtg	gacactctct	2100

tcttccttac caccgtgtgg acaaggcctg ggcccgaagt cctcaaccgc 2150  
 tgtcgcatga atgcatctc tggctggcag gccttcttcc cagtccattt 2200  
 ccaggagtcc aatcctgccc tgtcaccaca gagatcacc ccaggggccc 2250  
 cgggggctgg ccttgacccc cctccccc cttggtgctga cccctcccgg 2300  
 ggggctccta taggggggag atttgaccgg caggcttctg cggagggtg 2350  
 cttctacaac gctgactacc tggcggcccc agcccggtg gcaggatgaac 2400  
 tggcaggcca ggaagaggag gaagccctgg aggggctgga ggtgatggat 2450  
 gtttctctcc ggttctcagg gctccacctc ttccggggcc tagagccagg 2500  
 gctggtgcag aagttctccc tgcgagactg cagcccacgg ctcaagtgaag 2550  
 aactctacca ccgctgccgc ctcagcaacc tggaggggct agggggccgt 2600  
 gccagctgg ctatggctct ctttgagcag gagcaggcca atagcactta 2650  
 gccgcctgg gggccctaac ctcattacct ttcccttgct tgcctcagcc 2700  
 ccaggaaggg caaggcaaga tgggtggacag atagagaatt gttgctgtat 2750  
 tttttaaata tgaaaatggt attaaacatg tcttctgcc 2789

<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

Met	Arg	Leu	Ser	Ser	Leu	Leu	Ala	Leu	Leu	Arg	Pro	Ala	Leu	Pro
1					5					10				15

Leu	Ile	Leu	Gly	Leu	Ser	Leu	Gly	Cys	Ser	Leu	Ser	Leu	Leu	Arg
				20					25					30

Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala
				35					40					45

Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg
				50					55					60

Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr
				65					70					75

Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg
				80					85					90

Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

104420-354000

	95		100		105
Val Leu Thr Ser	Arg Ala Thr Leu Ser	Thr Leu Ala Val Ala Val			
	110	115			120
Asn Arg Thr Val	Ala His His Phe Pro	Arg Leu Leu Tyr Phe Thr			
	125	130			135
Gly Gln Arg Gly	Ala Arg Ala Pro Ala	Gly Met Gln Val Val Ser			
	140	145			150
His Gly Asp Glu	Arg Pro Ala Trp Leu	Met Ser Glu Thr Leu Arg			
	155	160			165
His Leu His Thr	His Phe Gly Ala Asp	Tyr Asp Trp Phe Phe Ile			
	170	175			180
Met Gln Asp Asp	Thr Tyr Val Gln Ala	Pro Arg Leu Ala Ala Leu			
	185	190			195
Ala Gly His Leu	Ser Ile Asn Gln Asp	Leu Tyr Leu Gly Arg Ala			
	200	205			210
Glu Glu Phe Ile	Gly Ala Gly Glu Gln	Ala Arg Tyr Cys His Gly			
	215	220			225
Gly Phe Gly Tyr	Leu Leu Ser Arg Ser	Leu Leu Leu Arg Leu Arg			
	230	235			240
Pro His Leu Asp	Gly Cys Arg Gly Asp	Ile Leu Ser Ala Arg Pro			
	245	250			255
Asp Glu Trp Leu	Gly Arg Cys Leu Ile	Asp Ser Leu Gly Val Gly			
	260	265			270
Cys Val Ser Gln	His Gln Gly Gln Gln	Tyr Arg Ser Phe Glu Leu			
	275	280			285
Ala Lys Asn Arg	Asp Pro Glu Lys Glu	Gly Ser Ser Ala Phe Leu			
	290	295			300
Ser Ala Phe Ala	Val His Pro Val Ser	Glu Gly Thr Leu Met Tyr			
	305	310			315
Arg Leu His Lys	Arg Phe Ser Ala Leu	Glu Leu Glu Arg Ala Tyr			
	320	325			330
Ser Glu Ile Glu	Gln Leu Gln Ala Gln	Ile Arg Asn Leu Thr Val			
	335	340			345
Leu Thr Pro Glu	Gly Glu Ala Gly Leu	Ser Trp Pro Val Gly Leu			
	350	355			360

Pro	Ala	Pro	Phe	Thr	Pro	His	Ser	Arg	Phe	Glu	Val	Leu	Gly	Trp
				365					370					375
Asp	Tyr	Phe	Thr	Glu	Gln	His	Thr	Phe	Ser	Cys	Ala	Asp	Gly	Ala
				380					385					390
Pro	Lys	Cys	Pro	Leu	Gln	Gly	Ala	Ser	Arg	Ala	Asp	Val	Gly	Asp
				395					400					405
Ala	Leu	Glu	Thr	Ala	Leu	Glu	Gln	Leu	Asn	Arg	Arg	Tyr	Gln	Pro
				410					415					420
Arg	Leu	Arg	Phe	Gln	Lys	Gln	Arg	Leu	Leu	Asn	Gly	Tyr	Arg	Arg
				425					430					435
Phe	Asp	Pro	Ala	Arg	Gly	Met	Glu	Tyr	Thr	Leu	Asp	Leu	Leu	Leu
				440					445					450
Glu	Cys	Val	Thr	Gln	Arg	Gly	His	Arg	Arg	Ala	Leu	Ala	Arg	Arg
				455					460					465
Val	Ser	Leu	Leu	Arg	Pro	Leu	Ser	Arg	Val	Glu	Ile	Leu	Pro	Met
				470					475					480
Pro	Tyr	Val	Thr	Glu	Ala	Thr	Arg	Val	Gln	Leu	Val	Leu	Pro	Leu
				485					490					495
Leu	Val	Ala	Glu	Ala	Ala	Ala	Ala	Pro	Ala	Phe	Leu	Glu	Ala	Phe
				500					505					510
Ala	Ala	Asn	Val	Leu	Glu	Pro	Arg	Glu	His	Ala	Leu	Leu	Thr	Leu
				515					520					525
Leu	Leu	Val	Tyr	Gly	Pro	Arg	Glu	Gly	Gly	Arg	Gly	Ala	Pro	Asp
				530					535					540
Pro	Phe	Leu	Gly	Val	Lys	Ala	Ala	Ala	Ala	Glu	Leu	Glu	Arg	Arg
				545					550					555
Tyr	Pro	Gly	Thr	Arg	Leu	Ala	Trp	Leu	Ala	Val	Arg	Ala	Glu	Ala
				560					565					570
Pro	Ser	Gln	Val	Arg	Leu	Met	Asp	Val	Val	Ser	Lys	Lys	His	Pro
				575					580					585
Val	Asp	Thr	Leu	Phe	Phe	Leu	Thr	Thr	Val	Trp	Thr	Arg	Pro	Gly
				590					595					600
Pro	Glu	Val	Leu	Asn	Arg	Cys	Arg	Met	Asn	Ala	Ile	Ser	Gly	Trp
				605					610					615
Gln	Ala	Phe	Phe	Pro	Val	His	Phe	Gln	Glu	Phe	Asn	Pro	Ala	Leu
				620					625					630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp  
 635 640 645  
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile  
 650 655 660  
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr  
 665 670 675  
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu  
 680 685 690  
 Ala Gly Gln Glu Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met  
 695 700 705  
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val  
 710 715 720  
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro  
 725 730 735  
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu  
 740 745 750  
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu  
 755 760 765  
 Gln Glu Gln Ala Asn Ser Thr  
 770

<210> 340

<211> 1572

<212> DNA

<213> Homo Sapien

<400> 340

cggagtgggtg cgccaacgtg agaggaaacc cgtgcgcggc tgcgctttcc 50  
 tgtccccaag ccgttctaga cgcgggaaaa atgctttctg aaagcagctc 100  
 ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150  
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200  
 catcatcacc tacaagctcc taacaaagaa gatattctga aaatttcaga 250  
 ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300  
 ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350  
 accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

gtttgagtca attaatatgg acacaaatga catgtgggta atgatgagaa 450  
 aagcttaciaa atacgccttt gataagtata gagaccaata caactgggttc 500  
 ttccttgcac gcccactac gtttgctatc attgaaaacc taaagtattt 550  
 tttgttaaaa aaggatccat cacagccttt ctatctaggc cacactataa 600  
 aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650  
 gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700  
 tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750  
 cagtttgcct gaaatatgct ggagtatttg cagaaaatgc agaagatgct 800  
 gatggaaaag atgtatttaa taccaaactc gttgggcttt ctattaaaga 850  
 ggcaatgact tatcacccca accaggtagt agaaggctgt tgttcagata 900  
 tggctgttac ttttaatgga ctgactccaa atcagatgca tgtgatgatg 950  
 tatgggggat accgccttag ggcatttggg catattttca atgatgcatt 1000  
 ggttttctta cctccaaatg gttctgacaa tgactgagaa gtggtagaaa 1050  
 agcgtgaata tgatctttgt ataggacgtg tgttgcatt atttgtagta 1100  
 gtaactacat atccaatata gctgtatggt tctttttctt ttctaatttg 1150  
 gtggcactgg tataaccaca cattaaagtc agtagtacat ttttaaataga 1200  
 ggggtggtttt tttctttaaa acacatgaac attgtaaatg tgttggaag 1250  
 aagtgtttta agaataataa ttttgcaaact aaactattaa taaatattat 1300  
 atgtgataaa ttctaaatta tgaacattag aaatctgtgg ggcacatatt 1350  
 tttgctgatt gggttaaaaaa ttttaacagg tcttttagcgt tctaagatat 1400  
 gcaaatgata tctctagttg tgaatttgtg attaaagtaa aacttttagc 1450  
 tgtgtgttcc ctttacttct aatactgatt tatgttctaa gcctccccaa 1500  
 gttccaatgg atttgccttc tcaaaatgta caactaagca actaaagaaa 1550  
 attaaagtga aagttgaaaa at 1572

<210> 341

<211> 318

<212> PRT

<213> Homo Sapien

000456.0340

&lt;400&gt; 341

Met	Leu	Ser	Glu	Ser	Ser	Ser	Phe	Leu	Lys	Gly	Val	Met	Leu	Gly	1	5	10	15
Ser	Ile	Phe	Cys	Ala	Leu	Ile	Thr	Met	Leu	Gly	His	Ile	Arg	Ile	20	25	30	
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln	35	40	45	
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg	50	55	60	
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val	65	70	75	
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp	80	85	90	
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val	95	100	105	
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu	110	115	120	
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp	125	130	135	
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile	140	145	150	
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln	155	160	165	
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr	170	175	180	
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys	185	190	195	
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln	200	205	210	
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val	215	220	225	
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala	230	235	240	
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile	245	250	255	
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys				

1  
 2  
 3  
 4  
 5  
 6  
 7  
 8  
 9  
 10  
 11  
 12  
 13  
 14  
 15  
 16  
 17  
 18  
 19  
 20  
 21  
 22  
 23  
 24  
 25  
 26  
 27  
 28  
 29  
 30  
 31  
 32  
 33  
 34  
 35  
 36  
 37  
 38  
 39  
 40  
 41  
 42  
 43  
 44  
 45  
 46  
 47  
 48  
 49  
 50  
 51  
 52  
 53  
 54  
 55  
 56  
 57  
 58  
 59  
 60  
 61  
 62  
 63  
 64  
 65  
 66  
 67  
 68  
 69  
 70  
 71  
 72  
 73  
 74  
 75  
 76  
 77  
 78  
 79  
 80  
 81  
 82  
 83  
 84  
 85  
 86  
 87  
 88  
 89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100  
 101  
 102  
 103  
 104  
 105  
 106  
 107  
 108  
 109  
 110  
 111  
 112  
 113  
 114  
 115  
 116  
 117  
 118  
 119  
 120  
 121  
 122  
 123  
 124  
 125  
 126  
 127  
 128  
 129  
 130  
 131  
 132  
 133  
 134  
 135  
 136  
 137  
 138  
 139  
 140  
 141  
 142  
 143  
 144  
 145  
 146  
 147  
 148  
 149  
 150  
 151  
 152  
 153  
 154  
 155  
 156  
 157  
 158  
 159  
 160  
 161  
 162  
 163  
 164  
 165  
 166  
 167  
 168  
 169  
 170  
 171  
 172  
 173  
 174  
 175  
 176  
 177  
 178  
 179  
 180  
 181  
 182  
 183  
 184  
 185  
 186  
 187  
 188  
 189  
 190  
 191  
 192  
 193  
 194  
 195  
 196  
 197  
 198  
 199  
 200  
 201  
 202  
 203  
 204  
 205  
 206  
 207  
 208  
 209  
 210  
 211  
 212  
 213  
 214  
 215  
 216  
 217  
 218  
 219  
 220  
 221  
 222  
 223  
 224  
 225  
 226  
 227  
 228  
 229  
 230  
 231  
 232  
 233  
 234  
 235  
 236  
 237  
 238  
 239  
 240  
 241  
 242  
 243  
 244  
 245  
 246  
 247  
 248  
 249  
 250  
 251  
 252  
 253  
 254  
 255  
 256  
 257  
 258  
 259  
 260  
 261  
 262  
 263  
 264  
 265  
 266  
 267  
 268  
 269  
 270  
 271  
 272  
 273  
 274  
 275  
 276  
 277  
 278  
 279  
 280  
 281  
 282  
 283  
 284  
 285  
 286  
 287  
 288  
 289  
 290  
 291  
 292  
 293  
 294  
 295  
 296  
 297  
 298  
 299  
 300  
 301  
 302  
 303  
 304  
 305  
 306  
 307  
 308  
 309  
 310  
 311  
 312  
 313  
 314  
 315  
 316  
 317  
 318  
 319  
 320  
 321  
 322  
 323  
 324  
 325  
 326  
 327  
 328  
 329  
 330  
 331  
 332  
 333  
 334  
 335  
 336  
 337  
 338  
 339  
 340  
 341  
 342  
 343  
 344  
 345  
 346  
 347  
 348  
 349  
 350  
 351  
 352  
 353  
 354  
 355  
 356  
 357  
 358  
 359  
 360  
 361  
 362  
 363  
 364  
 365  
 366  
 367  
 368  
 369  
 370  
 371  
 372  
 373  
 374  
 375  
 376  
 377  
 378  
 379  
 380  
 381  
 382  
 383  
 384  
 385  
 386  
 387  
 388  
 389  
 390  
 391  
 392  
 393  
 394  
 395  
 396  
 397  
 398  
 399  
 400



	260		265		270
Cys Ser Asp Met	Ala Val Thr Phe Asn Gly	Leu Thr Pro Asn Gln			
	275	280		285	
Met His Val Met	Met Tyr Gly Val Tyr Arg	Leu Arg Ala Phe Gly			
	290	295		300	
His Ile Phe Asn	Asp Ala Leu Val Phe Leu	Pro Pro Asn Gly Ser			
	305	310		315	

Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

tccccaagcc gttctagacg cgg 23

<210> 343

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 344

gccc aaatgc cctaaggcgg tatacccc 28

<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

For 20-3540600

<223> Synthetic Oligonucleotide Probe

<400> 345

gggtgtgatg cttggaagca ttttctgtgc tttgatcact atgctaggac 50

<210> 346

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 346

gggatgcagg tgggtgtctca tgggg 25

<210> 347

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 347

ccctcatgta ccggctcc 18

<210> 348

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 348

ggattctaatac gactcact atagggctca gaaaagcgca acagagaa 48

<210> 349

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 349

ctatgaaatt aaccctcact aaagggatgt cttccatgcc aaccttc 47

<210> 350

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 350

ggatttcta acgactcact atagggcggc gatgtccact ggggctac 48

<210> 351

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 351

ctatgaaatt aaccctcact aaagggacga ggaagatggg cggatggg 48

<210> 352

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 352

ggatttcta acgactcact atagggcacc cacgcgtcgg gctgctt 47

<210> 353

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 353

ctatgaaatt aaccctcact aaagggacgg gggacaccac ggaccaga 48

<210> 354

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 354

ggatttcta acgactcact atagggcttg ctgcggtttt tgttcctg 48

<210> 355

<211> 48

Top of sequence

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 355  
ctatgaaatt aaccctcact aaaggagct gccgatccca ctggtatt 48

<210> 356  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 356  
ggattctaatacgcactcact atagggcgga tcctggccgg cctctg 46

<210> 357  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 357  
ctatgaaatt aaccctcact aaaggagcc cgggcacgtt ctcagtta 48

<210> 358  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 358  
ggattctaatacgcactcact atagggcggg aagatggcga ggaggag 47

<210> 359  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 359  
ctatgaaatt aaccctcact aaaggaccca aggccacaaa cggaaatc 48

<210> 360  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 360  
ggattctaatacgcactcactatagggctgtgctttcattctgccagta 48

<210> 361  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 361  
ctatgaaattaacccctcactaaagggagggtacaattaaggggtggat 48

<210> 362  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 362  
ggattctaatacgcactcactatagggcccgccctcctcctgctcctg 47

<210> 363  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 363  
ctatgaaattaacccctcactaaagggaggattgccgcgaccctcacag 48

<210> 364  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 364

ggattctaatac gactcact atagggcccc tctgccttc cctgtcc 47

<210> 365

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 365

ctatgaaatt aaccctcact aaaggaggatg gtggccgcga ttatctgc 48

<210> 366

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 366

ggattctaatac gactcact atagggcgca gcatggcag cgatgagg 48

<210> 367

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 367

ctatgaaatt aaccctcact aaagggacag acggggcaga gggagtgc 47

<210> 368

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 368

ggattctaatac gactcact atagggccag gaggcgtgag gagaaac 47

<210> 369

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 369

ctatgaaatt aaccctcact aaagggaaaag acatgtcatc gggagtgg 48

<210> 370

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 370

ggatttctaatt acgactcact atagggcccg gtggaggtgg aacagaaa 48

<210> 371

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 371

ctatgaaatt aaccctcact aaagggacac agacagagcc ccatacgc 48

<210> 372

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 372

ggatttctaatt acgactcact atagggccag ggaaatccgg atgtctc 47

<210> 373

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 373

ctatgaaatt aaccctcact aaagggagta aggggatgcc accgagta 48

<210> 374

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 374

ggattctaatac gactcact atagggccag ctacccgcag gaggagg 47

<210> 375

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 375

ctatgaaatt aacctcact aaagggatcc caggtgatga ggtccaga 48

<210> 376

<211> 997

<212> DNA

<213> Homo Sapien

<400> 376

cccacgcgtc cgatcttacc aacaaaacac tcctgaggag aaagaaagag 50  
 agggagggag agaaaaagag agagagagaa acaaaaaacc aaagagagag 100  
 aaaaaatgaa ttcattctaaa tcattctgaaa cacaatgcac agagagagga 150  
 tgcttctctt cccaaatggt cttatggact gttgctggga tccccatcct 200  
 atttctcagt gctgttttca tcaccagatg tgttgatgaca tttcgcattct 250  
 ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300  
 ctctctgct acaattatgg atcaggttca gtcaagaatt gttgtccatt 350  
 gaactgggaa tatttttcaat ccagctgcta cttcttttct actgacacca 400  
 tttcctgggc gttaagttaa aagaactgct cagccatggg ggctcacctg 450  
 gtggttatca actcacagga ggagcaggaa ttcctttcct acaagaaacc 500  
 taaaatgaga gagtttttta ttggactgtc agaccagggt gtcgaggggtc 550  
 agtggcaatg ggtggacggc acacctttga caaagtctct gagcttcttg 600  
 gatgtagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650  
 gagagactct tcaaaccxaa ggcaaaattg gaatgatgta acctgtttcc 700  
 tcaattattt tcggatttgt gaaatggtag gaataaatcc tttgaacaaa 750

For "9564066"



ggaaaatctc tttaagaaca gaaggcacia ctcaaattgtg taaagaagga 800  
 agagcaagaa catggccaca cccaccgccc cacacgagaa atttgtgcgc 850  
 tgaacttcaa aggacttcat aagtatttgt tactctgata caaataaaaa 900  
 taagtagttt taaatgttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 950  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 997

<210> 377

<211> 219

<212> PRT

<213> Homo Sapien

<400> 377

Met	Asn	Ser	Ser	Lys	Ser	Ser	Glu	Thr	Gln	Cys	Thr	Glu	Arg	Gly	1	5	10	15
Cys	Phe	Ser	Ser	Gln	Met	Phe	Leu	Trp	Thr	Val	Ala	Gly	Ile	Pro	20	25	30	
Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr	35	40	45	
Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro	50	55	60	
Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser	65	70	75	
Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser	80	85	90	
Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu	95	100	105	
Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser	110	115	120	
Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg	125	130	135	
Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp	140	145	150	
Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp	155	160	165	
Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala	170	175	180	

for seqs

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val  
 185 190 195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile  
 200 205 210

Asn Pro Leu Asn Lys Gly Lys Ser Leu  
 215

<210> 378

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 378

ttcagcttct gggatgtagg g 21

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 379

tattcctacc atttcacaaa tccg 24

<210> 380

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

ggaggactgt gccaccatga gagactcttc aaaccaagg caaaattgg 49

<210> 381

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 381

gcagattttg aggacagcca cctcca 26

0904056 07404

<210> 382  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 382  
ggccttgcag acaaccgt 18

<210> 383  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 383  
cagactgagg gagatccgag a 21

<210> 384  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 384  
cagctgccct tccccaacca 20

<210> 385  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 385  
catcaagcgc ctctacca 18

<210> 386  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 386

```
<210> 387
<211> 18
<212> DNA
<213> Artificial Sequence
```

```
<400> 387
   gggccatcac agctccct 18
```

<220>  
<223> Synthetic oligonucleotide probe

```
<210> 389
<211> 22
```

<220>  
<223> Synthetic oligonucleotide probe

```
<210> 390
<211> 20
<212> DNA
<213> Artificial Sequence
```

<400> 390  
cagaaggatg tcccgtaggaa 20

<220>

<223> Synthetic oligonucleotide probe

<400> 391

gccgctgtcc actgcag 17

<210> 392

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

gacggcatcc tcagggccac a 21

<210> 393

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

atgtcctcca tgcccacgcg 20

<210> 394

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 394

gagtgcgaca tcgagagctt 20

<210> 395

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 395

ccgcagcctc agtgatga 18

<210> 396

<211> 21

<212> DNA

<213> Artificial Sequence

FOR SEQUENCE

<220>  
<223> Synthetic oligonucleotide probe

<400> 396  
gaagagcaca gctgcagatc c 21

<210> 397  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 397  
gaggtgtcct ggctttggta gt 22

<210> 398  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 398  
cctctggcgc cccactcaa 20

<210> 399  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 399  
ccaggagagc tggcgatg 18

<210> 400  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 400  
gcaaattcag ggctcactag aga 23

<210> 401  
<211> 29

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 401  
cacagagcat ttgtccatca gcagttcag 29

<210> 402  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 402  
ggcagagact tccagtcact ga 22

<210> 403  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 403  
gccaaaggggtg gtgtagata gg 22

<210> 404  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 404  
caggccccct tgatctgtac ccca 24

<210> 405  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 405  
gggacgtgct tctacaagaa cag 23

<210> 406  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 406  
 caggettaca atgttatgat cagaca 26  
  
 <210> 407  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 407  
 tattcagagt tttccattgg cagtgccagt t 31  
  
 <210> 408  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 408  
 tctacatcag cctctctgcg c 21  
  
 <210> 409  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 409  
 cgatcttctc caccagag cg 23  
  
 <210> 410  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 410



```

<210> 411
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 411
ctccctgaat ggcagcctga gca 23

<210> 412
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 412
aggtgtttat taagggccta cgct 24

<210> 413
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 413
cagagcagag ggtgccttg 19

<210> 414
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 414
tggcggagtc ccctcttggc t 21

<210> 415
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

```

<223> Synthetic oligonucleotide probe

<400> 415

ccctgtttcc ctatgcatca ct 22

<210> 416

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 416

tcaaccctg accctttcct a 21

<210> 417

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 417

ggcaggggac aagccatctc tcct 24

<210> 418

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

gggactgaac tgccagcttc 20

<210> 419

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 419

gggccctaac ctcattacct tt 22

<210> 420

<211> 23

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 420  
 tgtctgcctc agccccagga agg 23

<210> 421  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 421  
 tctgtccacc atcttgctt g 21

<210> 422  
 <211> 3554  
 <212> DNA  
 <213> Homo Sapien

<400> 422  
 gggactacaa gccgcgcgc gctgccgctg gccctcagc aaccctcgac 50  
 atggcgctga ggcggccacc gcgactccgg ctctgcgctc ggctgcctga 100  
 cttcttctctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150  
 tcaaattccag caatcgaacc ccagtggtag aggaatttga aagtgtggaa 200  
 ctgtcttgca tcattacgga ttcgcagaca agtgacccca ggatcgagt 250  
 gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300  
 ttcagggaga cttggcgggt cgtgcagaaa tactggggaa gacatccctg 350  
 aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400  
 cgttgctcga aatgaccgca aggaaattga tgagattgtg atcgagttaa 450  
 ctgtgcaagt gaagccagtg acccctgtct gtagagtgcc gaaggctgta 500  
 ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550  
 ccggcctcac tacagctggg atcgcaatga tgtaccactg cccacggatt 600  
 ccagagccaa tcccagattt cgcaattctt ctttccactt aaactctgaa 650  
 acaggcactt tgggtgttcac tgctgttcac aaggacgact ctgggcagta 700  
 ctactgcatt gcttccaatg acgcaggctc agccaggtgt gaggagcagg 750

090455 074401



agatggaagt ctatgacctg aacattggcg gaattattgg gggggttctg 800  
gttgtccttg ctgtactggc cctgatcacg ttgggcatct gctgtgcata 850  
cagacgtggc tacttcatca acaataaaca ggatggagaa agttacaaga 900  
accagggaa accagatgga gttaactaca tccgcactga cgaggagggc 950  
gacttcagac acaagtcacg gtttgtgatc tgagaccgcg ggtgtggctg 1000  
agagcgcaca gagcgacgt gcacatacct ctgctagaaa ctctgtcaa 1050  
ggcagcgaga gctgatgcac tcggacagag ctagacactc attcagaagc 1100  
ttttcgtttt ggccaaagtt gaccactact cttcttactc taacaagcca 1150  
catgaataga agaattttcc tcaagatgga cccggtaaata ataaccacaa 1200  
ggaagcgaaa ctgggtgcgt tcaactgagtt gggttcctaa tctgtttctg 1250  
gcctgattcc cgcattgagta ttagggatgat cttaaagagt ttgctcacgt 1300  
aaacgcccgt gctgggccct gtgaagccag catgttcacc actggctcgtt 1350  
cagcagccac gacagcacca tgtgagatgg cgaggtggct ggacagcacc 1400  
agcagcgcct cccggcgagg acccagaaaa ggcttcttac acagcagcct 1450  
tacttcatcg gccacagac accaccgcag tttcttctta aaggctctgc 1500  
tgatcgggtg tgcagtgtcc attgtggaga agctttttgg atcagcattt 1550  
tgtaaaaaca accaaaatca ggaaggtaaa ttggttgctg gaagagggat 1600  
cttgctgag gaacctgct tgtccaacag ggtgtcagga ttttaaggaaa 1650  
accttcgtct taggctaagt ctgaaatggc actgaaatat gcttttctat 1700  
gggtcttggt tattttataa aattttacat cttaaatttt gctaaggatg 1750  
tattttgatt attgaaaaga aaatttctat ttaaactgta aatatattgt 1800  
catacaatgt taaataacct atttttttta aaaagtcca ctttaaggtag 1850  
aagttccaag ctactagtgt taaattggaa aatatcaata attaagagta 1900  
ttttacccaa ggaatcctct catggaagtt tactgtgatg ttccctttct 1950  
cacacaagtt ttagcctttt tcacaaggga actcatactg tctacacatc 2000  
agaccatagt tgcttaggaa acctttaaaa attccagtta agcaatgttg 2050

T0440"990600

aaatcagttt gcatctcttc aaaagaaacc tctcaggtta gctttgaact 2100  
 gcctcttctt gagatgacta ggacagtctg taccagagg ccaccagaa 2150  
 gccctcagat gtacatacac agatgccagt cagctcctgg ggttgcgcca 2200  
 ggcgcccccg ctctagctca ctgttgctc gctgtctgcc aggaggccct 2250  
 gccatccttg gccctggca gtggctgtgt cccagtgagc ttactcacg 2300  
 tggccttgcc ttcattccagc acagctctca ggtgggcact gcaggacac 2350  
 tgggtgtctt catgtagcgt cccagctttg ggctcctgta acagacctct 2400  
 ttttggttat ggatggctca caaaataggg ccccaatgc ttttttttt 2450  
 ttttaagttt gtttaattat ttgttaagat tgtctaaggc caaaggcaat 2500  
 tgcgaaatca agtctgtcaa gtacaataac atttttaaaa gaaaatggat 2550  
 cccactgttc ctctttgcca cagagaaagc acccagacgc cacaggctct 2600  
 gtgcgatttc aaaacaaacc atgatggagt ggcggccagt ccagcctttt 2650  
 aaagaacgtc aggtggagca gccaggtgaa aggcctggcg gggaggaaag 2700  
 tgaaacgcct gaatcaaaag cagttttcta attttgactt taaatttttc 2750  
 atccgcgga gacactgtc ccatttgtgg ggggacatta gcaacatcac 2800  
 tcagaagcct gtgttcttca agagcagggtg ttctcagcct cacatgccct 2850  
 gccgtgctgg actcaggact gaagtgtgt aaagcaagga gctgctgaga 2900  
 aggagcactc cactgtgtgc ctggagaatg gctctcacta ctcacctgt 2950  
 ctttcagctt ccagtgtctt gggtttttta tactttgaca gctttttttt 3000  
 aattgcatac atgagactgt gttgactttt tttagttatg tgaaacactt 3050  
 tgccgcaggc cgctggcag aggcaggaaa tgctccagca gtggctcagt 3100  
 gctccctggg gtctgctgca tggcatcctg gatgcttagc atgcaagttc 3150  
 cctccatcat tgccaccttg gtagagaggg atggctcccc accctcagcg 3200  
 ttggggattc acgctccagc ctcttcttgg gttgtcatag tgatagggt 3250  
 gccttattgc cccctcttct tataacctaa aaccttctac actagtgcc 3300  
 tgggaaccag gtctgaaaaa gtagagagaa gtgaaagtag agtctgggaa 3350  
 gtagctgcct ataactgaga ctagacggaa aaggaatact cgtgtatttt 3400

aagatatgaa tgtgactcaa gactcgaggc cgatacgagg ctgtgattct 3450  
gcctttggat ggatgttgct gtacacagat gctacagact tgtactaaca 3500  
caccgtaatt tggcatttgt ttaacctcat ttataaaaagc ttcaaaaaaa 3550  
ccca 3554

<210> 423

<211> 310

<212> PRT

<213> Homo Sapien

<400> 423

Met	Ala	Leu	Arg	Arg	Pro	Pro	Arg	Leu	Arg	Leu	Cys	Ala	Arg	Leu	1	5	10	15
Pro	Asp	Phe	Phe	Leu	Leu	Leu	Leu	Phe	Arg	Gly	Cys	Leu	Ile	Gly	20	25	30	
Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu	35	40	45	
Phe	Glu	Ser	Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	Asp	Ser	Gln	Thr	50	55	60	
Ser	Asp	Pro	Arg	Ile	Glu	Trp	Lys	Lys	Ile	Gln	Asp	Glu	Gln	Thr	65	70	75	
Thr	Tyr	Val	Phe	Phe	Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly	80	85	90	
Arg	Ala	Glu	Ile	Leu	Gly	Lys	Thr	Ser	Leu	Lys	Ile	Trp	Asn	Val	95	100	105	
Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg	110	115	120	
Asn	Asp	Arg	Lys	Glu	Ile	Asp	Glu	Ile	Val	Ile	Glu	Leu	Thr	Val	125	130	135	
Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val	140	145	150	
Pro	Val	Gly	Lys	Met	Ala	Thr	Leu	His	Cys	Gln	Glu	Ser	Glu	Gly	155	160	165	
His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn	Asp	Val	Pro	Leu	170	175	180	
Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe	185	190	195	

for 2095666

100-443886-100